

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 07:30:54 ; Search time 1527.67 Seconds

(without alignments)
566.880 Million cell updates/sec

Title: US-09-310-844c-24

Perfect score: 29
Sequence: 1 uagauuuuuuuuagccuagggggu 29

Scoring table: IDENTITY NUC

Gapop 10'0 , Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 375216

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

EST:

1: em_estba:*
2: em_estum:*
3: em_estin:*
4: em_estu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hc:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.2	55.9	57	9	AI561770
2	16.2	55.9	77	14	CB262321
3	16	55.2	77	28	BH252676
4	15.4	53.1	61	29	CG590967

66	29	TA123H02P	53.1	15.4	53.1	BM568281	T. brucei
73	12	BM568281	53.1	15.4	53.1	sal02d02	
41	14	CB210991	52.4	15.2	52.4	OML01271	
63	29	EX533881	52.4	15.2	52.4	Arabidops	
69	29	CG734697	52.4	15.2	52.4	1119150C1	
25	28	AZ993079	51.0	14.8	51.0	BE871815	
60	10	BE871815	51.0	14.8	51.0	601447803	
64	29	EX003595	51.0	14.8	51.0	Arabidops	
66	14	CD925111	51.0	14.8	51.0	G750_1150	
69	12	BM128463	51.0	14.8	51.0	if15c05.x	
72	28	BZ763921	51.0	14.8	51.0	SAUK_1227	
72	29	TA185E01P	51.0	14.8	51.0	AL74065	T. brucei
73	28	AZ775013	51.0	14.8	51.0	2M0004K20	
74	9	AI819570	51.0	14.8	51.0	wj91308.x	
76	9	AA975663	51.0	14.8	51.0	qg63f07.s	
76	12	BI963697	51.0	14.8	51.0	ie63a09.x	
76	28	AZ657549	51.0	14.8	51.0	1M0533118	
77	29	CG545254	50.3	14.6	50.3	OST152329	
49	29	BX287070	50.3	14.6	50.3	Arabidops	
52	12	BG236504	50.3	14.6	50.3	na144c06	
62	28	BH911891	50.3	14.6	50.3	na144c06	
63	29	CG563472	50.3	14.6	50.3	SALK_0727	
64	9	AI139668	50.3	14.6	50.3	QC28h07.x	
64	28	AZ808107	50.3	14.6	50.3	2M0071024	
66	28	AZ40181	50.3	14.6	50.3	1M0231810	
73	12	BI865610	50.3	14.6	50.3	ft22h02.y	
73	29	EX001193	50.3	14.6	50.3	Arabidops	
79	14	D11626	50.3	14.6	50.3	HUM0C13G12	
31	28	BH910631	49.7	14.4	49.7	SALK_0607	
43	28	AZ597048	49.7	14.4	49.7	1M0410K10	
44	29	AL771575	49.7	14.4	49.7	Arabidops	
54	12	BI865449	49.7	14.4	49.7	ft22h02.x	
60	9	AI595218	49.7	14.4	49.7	AL595218	
63	12	BG362434	49.7	14.4	49.7	gb72b09.y	
65	29	CG664319	49.7	14.4	49.7	OST451176	
67	9	AI584052	49.7	14.4	49.7	ts13b02.x	
67	10	BE027305	49.7	14.4	49.7	EtBStea89	
67	28	BZ289657	49.7	14.4	49.7	SALK_0230	
68	29	CG581901	49.7	14.4	49.7	OST222599	
69	10	BE647308	49.7	14.4	49.7	UI-M-BH1-	
76	9	AI300666	49.7	14.4	49.7	qo22a12.x	
52	10	AW686481	49.0	14.2	49.0	qo22a12.x	
59	28	B00509	49.0	14.2	49.0	CSRL-115b2-	
61	9	AI318033	49.0	14.2	49.0	ta75g02.x	
67	29	EX004510	49.0	14.2	49.0	Arabidops	
70	13	B0063954	49.0	14.2	49.0	Fgr_3_M18	
72	13	BQ613481	49.0	14.2	49.0	rd07h06.y	
75	29	CG526082	49.0	14.2	49.0	OST102290	
76	29	CG781030	49.0	14.2	49.0	1123043A0	
76	29	BX895575	49.0	14.2	49.0	Arabidops	
52	10	BP637245	48.3	14	48.3	NP002F08L	
65	12	BI094834	48.3	14	48.3	EST-CD34N	
67	9	AA936041	48.3	14	48.3	nz53f10.s	
67	28	BH855810	48.3	14	48.3	SAUK_0845	
73	14	CD942294	48.3	14	48.3	RBR_27_Ge	
76	29	AL757078	48.3	14	48.3	Arabidops	
79	28	AQ073107	48.3	14	48.3	EP(3)3672	
80	29	AB082353	48.3	14	48.3	Drosophil	
37	23	AL931243	47.6	13.8	47.6	Arabidops	
39	28	BH909815	47.6	13.8	47.6	SAUK_0561	
40	28	BH857340	47.6	13.8	47.6	SAUK_0764	
40	28	BH857342	47.6	13.8	47.6	SAUK_0764	
40	29	CG779591	47.6	13.8	47.6	1123034H1	
43	28	AZ484548	47.6	13.8	47.6	1M0311N02	
55	9	AT005996	47.6	13.8	47.6	AT005996	
55	9	AA276988	47.6	13.8	47.6	va25g03.x	
64	29	AL770628	47.6	13.8	47.6	Arabidops	
65	29	CG507905	47.6	13.8	47.6	OST58111	
65	29	AL763793	47.6	13.8	47.6	Arabidops	
66	29	AL767936	47.6	13.8	47.6	Arabidops	
67	29	CG598850	47.6	13.8	47.6	ni17d07.s	
70	9	AA922973	47.6	13.8	47.6	OST240321	
70	9	AA922973	47.6	13.8	47.6	ok77e01.s	

C	78	13.8	47.6	70	9	AA516989	vh89d02.r	151	13.4	46.2	76	12	BG151596	na6giho7.
	79	13.8	47.6	71	10	BE320887	NFO28A06R	C 152	13.4	46.2	76	28	BZ290783	BZ290783 SALK 0914
	80	13.8	47.6	72	28	CC458528	SALK 1194	C 153	13.4	46.2	77	10	AW698377	AW698377 G223 G1an
	81	13.8	47.6	73	29	CC507904	OST58109	C 154	13.4	46.2	79	14	W89294	W89294 mf62h03.r1
	82	13.8	47.6	76	29	CC650582	OST5429400	C 155	13.2	45.5	28	28	AZ379665	AZ379665 1M0134019
	83	13.8	47.6	77	13	BQ100875	1j25a03.x	C 156	13.2	45.5	33	9	AU256066	AU256066 AU256066
	84	13.8	47.6	78	9	AL593367	AL593367	C 157	13.2	45.5	34	28	AZ776073	AZ776073 2M0009W20
	85	13.8	47.6	78	14	CK101830	F122P85.5	C 158	13.2	45.5	34	29	BX001854	BX001854 Arabidops
	86	13.8	47.6	78	14	CK108462	I018P45.P	C 159	13.2	45.5	50	9	AL005680	AL005680 AU105680
	87	13.8	47.6	78	14	CK108462	I018P45.P	C 160	13.2	45.5	52	28	BZ662046	BZ662046 SALK 0255
	88	13.8	47.6	80	29	AL948895	Arabidops	C 161	13.2	45.5	53	28	AZ376460	AZ376460 1M0130017
	89	13.6	46.9	80	29	AL770832	Arabidops	C 162	13.2	45.5	55	28	BZ288871	BZ288871 SALK 0222
	90	13.6	46.9	22	14	D18745	MUSGS01807	C 163	13.2	45.5	56	28	AZ938752	AZ938752 2M0137N19
	91	13.6	46.9	39	13	BX556938	BX556938	C 164	13.2	45.5	57	9	AA584628	AA584628 nc12808.s
	92	13.6	46.9	42	14	CF294887	3ODGS--04	C 165	13.2	45.5	58	9	AI824019	AI824019 WJ29f03.x
	93	13.6	46.9	47	9	AU254247	AU254247	C 166	13.2	45.5	59	9	AL930881	AL930881 AU930881
	94	13.6	46.9	49	10	BE970036	BE970036	C 167	13.2	45.5	59	9	AU256410	AU256410 AU256410
	95	13.6	46.9	50	9	AU104386	AU104386	C 168	13.2	45.5	61	12	BI793571	BI793571 1c40H02.X
	96	13.6	46.9	50	12	BI942315	sh06a05.Y	C 169	13.2	45.5	61	29	CG582542	CG582542 OST223810
	97	13.6	46.9	56	28	BH906957	SALK 0368	C 170	13.2	45.5	61	29	CG582542	CG582542 OST223810
	98	13.6	46.9	58	13	BQ586792	E012390-0	C 171	13.2	45.5	61	29	CG523257	CG523257 OST234636
	99	13.6	46.9	58	29	BX893207	Arabidops	C 172	13.2	45.5	62	29	CG559308	CG559308 OST178029
	100	13.6	46.9	61	12	BM123335	L0523C08-	C 173	13.2	45.5	64	9	AI139668	AI139668 Q28h07.x
	101	13.6	46.9	62	10	B8647045	UI-M-BH1-	C 174	13.2	45.5	64	10	AW874915	AW874915 SWYACAL04
	102	13.6	46.9	65	9	AI960274	sc81c01.Y	C 175	13.2	45.5	65	9	AI019809	AI019809 ua93C08.r
	103	13.6	46.9	65	29	CG610825	OST294984	C 176	13.2	45.5	65	14	CD946488	CD946488 REO 34 Ge
	104	13.6	46.9	67	28	AZ760573	1M055124	C 177	13.2	45.5	65	29	CG708273	CG708273 1119008C1
	105	13.6	46.9	67	28	CC458056	SALK_1154	C 178	13.2	45.5	66	28	AZ471060	AZ471060 1M0285002
	106	13.6	46.9	68	9	AI903016	QV-ET022-	C 179	13.2	45.5	67	9	AA708911	AA708911 z164a10.s
	107	13.6	46.9	68	14	CD682098	rj46c08.Y	C 180	13.2	45.5	67	13	BQ243692	BQ243692 TaE15010F
	108	13.6	46.9	72	9	AA682755	ah52f07.s	C 181	13.2	45.5	68	28	AZ665787	AZ665787 1M0547123
	109	13.6	46.9	72	9	AI900474	sc11b10.Y	C 182	13.2	45.5	68	29	CG644709	CG644709 OST388378
	110	13.6	46.9	73	9	AA661115	WZ6SH11.X	C 183	13.2	45.5	69	28	AZ456041	AZ456041 1M0258J10
	111	13.6	46.9	73	28	AZ920626	1060602G0	C 184	13.2	45.5	71	9	AA789166	AA789166 ag58b03.s
	112	13.6	46.9	78	12	BM515022	Kx95a08.Y	C 185	13.2	45.5	71	29	AG264184	AG264184 Lotus cor
	113	13.4	46.2	34	29	TA98E04P	AL461231 T. brucei	C 186	13.2	45.5	72	28	AZ776513	AZ776513 2M0010M10
	114	13.4	46.2	45	29	AL761592	Arabidops	C 187	13.2	45.5	74	28	BH789670	BH789670 SALK_0433
	115	13.4	46.2	48	28	B2596082	B2596082 SALK 0920	C 188	13.2	45.5	75	12	BG362263	BG362263 g975f05.Y
	116	13.4	46.2	50	9	AI960055	sc37e07.x	C 189	13.2	45.5	75	29	CG618181	CG618181 OST312509
	117	13.4	46.2	50	28	BZ289491	SALK_0228	C 190	13.2	45.5	75	29	AL754690	AL754690 Arabidops
	118	13.4	46.2	52	9	AU258888	AU258888	C 191	13.2	45.5	76	13	BQ336895	BQ336895 STEM2.18
	119	13.4	46.2	53	10	BF637089	NFO50F04L	C 192	13.2	45.5	76	13	BQ336895	BQ336895 STEM2.18
	120	13.4	46.2	53	29	BX660051	Arabidops	C 193	13.2	45.5	76	13	BQ336895	BQ336895 STEM2.18
	121	13.4	46.2	56	12	BG231426	BG231426 nai42f02.	C 194	13.2	45.5	77	13	BG652110	BG652110 1112097E1
	122	13.4	46.2	58	28	B02943	CSRL-16302-	C 195	13.2	45.5	77	29	AL944740	AL944740 Arabidops
	123	13.4	46.2	59	9	AI651430	wa22b08.x	C 196	13.2	45.5	78	9	AA498911	AA498911 v183D06.r
	124	13.4	46.2	59	29	AL766549	Arabidops	C 197	13.2	45.5	78	28	BH252197	BH252197 SALK 0129
	125	13.4	46.2	61	14	CD984792	QAM25f05.	C 198	13.2	45.5	79	14	CD582985	CD582985 x129a04.Y
	126	13.4	46.2	62	10	BF470295	UI-M-BH3-	C 199	13.2	45.5	79	28	AZ336769	AZ336769 1M0067L12
	127	13.4	46.2	63	12	BG362361	gb70h04.Y	C 200	13.2	45.5	80	29	CG474696	CG474696 OST2739.M
	128	13.4	46.2	63	14	CB932680	CB932680 rj05g06.Y	C 201	13.4	44.8	27	2	FSM003610	FSM003610 Homo sapi
	129	13.4	46.2	63	29	CG598969	CG598969 OST264706	C 202	13.4	44.8	27	28	BH909838	BH909838 SALK_0561
	130	13.4	46.2	64	9	AA935784	AA935784	C 203	13.4	44.8	29	29	TA294B05P	TA294B05P Homo sapi
	131	13.4	46.2	64	28	AZ509948	1M0354E07	C 204	13.4	44.8	30	2	FSM001042	FSM001042 Homo sapi
	132	13.4	46.2	64	29	BX291940	BX291940 Arabidops	C 205	13.4	44.8	30	2	FSM001581	FSM001581 Homo sapi
	133	13.4	46.2	65	9	AA620913	af96b03.s	C 206	13.4	44.8	32	2	FSM001595	FSM001595 Homo sapi
	134	13.4	46.2	67	13	CB761969	BX761969	C 207	13.4	44.8	32	2	FSM001674	FSM001674 Homo sapi
	135	13.4	46.2	67	14	CB165153	CB165153 86 Alfalf	C 208	13.4	44.8	33	2	FSM003086	FSM003086 Homo sapi
	136	13.4	46.2	69	9	AI211081	noe06al.f	C 209	13.4	44.8	33	2	FSM003165	FSM003165 Homo sapi
	137	13.4	46.2	70	9	AI609394	AI609394 TW93B03.X	C 210	13.4	44.8	33	9	AL048719	AL048719 DKEP2566G
	138	13.4	46.2	70	9	AV916602	AV916602	C 211	13.4	44.8	33	9	AL048719	AL048719 DKEP2566G
	139	13.4	46.2	71	12	BM873635	BM873635 laa01a12.	C 212	13.4	44.8	34	2	FSM003069	FSM003069 Homo sapi
	140	13.4	46.2	71	14	CK109829	N029E03.P	C 213	13.4	44.8	34	2	FSM001818	FSM001818 Homo sapi
	141	13.4	46.2	72	13	BU744002	BU744002 mah94e12.	C 214	13.4	44.8	42	28	BZ661965	BZ661965 SALK 0254
	142	13.4	46.2	72	28	AZ760023	AZ760023 1M0553F22	C 215	13.4	44.8	42	28	AZ637149	AZ637149 1M0496F19
	143	13.4	46.2	72	29	CG780334	CG780334 1123039A0	C 216	13.4	44.8	44	9	AU008189	AU008189 Arabidops
	144	13.4	46.2	73	12	BM889450	BM889450 laa01a12.	C 217	13.4	44.8	44	29	AL753209	AL753209 Arabidops
	145	13.4	46.2	74	28	AZ986310	AZ986310 2M0268024	C 218	13.4	44.8	46	9	AI680115	AI680115 tw65a03.x
	146	13.4	46.2	74	28	BH642955	BH642955 1008050B0	C 219	13.4	44.8	46	9	AI103611	AI103611 AU103611
	147	13.4	46.2	74	29	CG574740	CG574740 OST207881	C 220	13.4	44.8	50	29	AL752392	AL752392 Arabidops
	148	13.4	46.2	74	29	CG723421	CG723421 1119076C1	C 221	13.4	44.8	52	10	AW245287	AW245287 2820140.3
	149	13.4	46.2	75	14	H07686	H07686 kbge012.BNL	C 222	13.4	44.8	53	2	FSM002757	FSM002757 Homo sapi
	150	13.4	46.2	75	28	AZ453746	AZ453746 1M0255A23	C 223	13.4	44.8	54	29	CC886314	CC886314 SALK_1516

224	13	44.8	55	28	AZ505773	IM0346B08	AZ505773	1M0346B08	60	13	BQ548512	rd12910.Y
225	13	44.8	55	29	BX148741	Danio rer	BX148741	Danio rer	60	29	CG865953	XP0393.Sa
226	13	44.8	57	29	AL758068	Arabidops	AL758068	Arabidops	61	29	CG723930	1119078G0
227	13	44.8	58	28	BZ290442	SALK_0238	BZ290442	SALK_0238	62	29	CG715132	1119040A1
228	13	44.8	58	29	AL948765	Arabidops	AL948765	Arabidops	63	12	BG362029	GBS060ell.Y
229	13	44.8	60	10	BF634030	NF072H10D	BF634030	NF072H10D	64	9	AI864772	wk02109.X
230	13	44.8	60	13	BX714486	BX714486	BX714486	BX714486	64	9	AA388420	vc95a03.r
231	13	44.8	61	9	AI363965	QW34606.X	AI363965	QW34606.X	64	10	BE638263	SMOV3MCMAR
232	13	44.8	61	28	AZ776619	2M0010E21	AZ776619	2M0010E21	64	10	BF154339	SMOV3MCMAR
233	13	44.8	63	9	AU258895	AU258895	AU258895	AU258895	64	10	BF154377	SMOV3MCMAR
234	13	44.8	64	9	AU254470	QW47H04.X	AU254470	QW47H04.X	64	10	CG570212	OST198924
235	13	44.8	64	29	CG497098	OST37528	CG497098	OST37528	64	29	EX531796	Arabidops
236	13	44.8	65	2	HS0001786	Al037455 Homo sapi	AL037455	Homo sapi	65	9	AI279493	ql51a01.X
237	13	44.8	65	9	AA733449	vt73H08.r	AA733449	vt73H08.r	65	12	BG361984	GB46910.Y
238	13	44.8	65	13	AI744319	tr09040.X	AI744319	tr09040.X	65	14	CF292099	14R00T--0
239	13	44.8	65	13	BX735697	BX735697	BX735697	BX735697	66	9	AL898170	AL898170
240	13	44.8	65	29	CG711452	1119021E0	CG711452	1119021E0	66	9	AA247859	j3371.seq
241	13	44.8	65	29	AL768493	Arabidops	AL768493	Arabidops	66	14	NS8453	y71102.81
242	13	44.8	67	29	AI271601	QW8410.X	AI271601	QW8410.X	67	14	NS8453	y71102.81
243	13	44.8	68	9	AA826444	oe66a01.s	AA826444	oe66a01.s	67	28	BH848343	
244	13	44.8	68	13	BQ476462	curculio5	BQ476462	curculio5	67	29	CG725431	1119085D0
245	13	44.8	68	14	CD941137	ir39a07.Y	CD941137	ir39a07.Y	68	9	AU014537	AU014537
246	13	44.8	68	14	CD942008	RRM_5 Gen	CD942008	RRM_5 Gen	68	28	AZ575904	AST-T32B0
247	13	44.8	68	14	CD949759	SAN_18 Ge	CD949759	SAN_18 Ge	68	29	CG547926	OST149074
248	13	44.8	68	14	CD950134	SAP_14 Ge	CD950134	SAP_14 Ge	68	29	CG547926	OST149074
249	13	44.8	68	29	CG485884	OST30540	CG485884	OST30540	68	29	CG660730	OST448854
250	13	44.8	68	29	CG473498	OST370475	CG473498	OST370475	68	29	CG721789	1119069A0
251	13	44.8	69	29	CG474384	OST2336.M	CG474384	OST2336.M	69	29	AL770150	Arabidops
252	13	44.8	70	12	BG115213	602316124	BG115213	602316124	70	12	BG360951	GB42b12.Y
253	13	44.8	70	29	CG581815	OST2322428	CG581815	OST2322428	70	29	CG615091	OST304148
254	13	44.8	72	13	BX760291	BX760291	BX760291	BX760291	71	14	CF800832	r168c12.Y
255	13	44.8	72	14	N85267	J3025F.Huma	N85267	J3025F.Huma	71	29	CG520384	OST85614
256	13	44.8	73	12	BZ361878	GB46b10.Y	BZ361878	GB46b10.Y	71	29	AL939770	Arabidops
257	13	44.8	73	14	CK097081	UB38BPC12	CK097081	UB38BPC12	72	29	CG628578	OST339790
258	13	44.8	73	18	AZ774350	2M0003C08	AZ774350	2M0003C08	73	10	BE570193	601331740
259	13	44.8	73	24	BX285024	Arabidops	BX285024	Arabidops	73	12	BM884177	rc20b06.Y
260	13	44.8	74	14	CD573927	fe05g01.X	CD573927	fe05g01.X	74	13	BQ591165	S013311-0
261	13	44.8	74	14	N85267	J3025F.Huma	N85267	J3025F.Huma	74	14	D19528	MUGS009322
262	13	44.8	74	29	AL760144	Arabidops	AL760144	Arabidops	74	29	CG667990	OST463127
263	13	44.8	74	29	BX288681	Arabidops	BX288681	Arabidops	75	10	AW516157	xt61g04.X
264	13	44.8	76	29	BX392165	Arabidops	BX392165	Arabidops	76	13	BQ977572	QHT2F06.Y
265	13	44.8	77	9	AA743582	nv29c01.s	AA743582	nv29c01.s	76	28	AZ591864	IM0402G15
266	13	44.8	77	10	AW460213	hh56e03.Y	AW460213	hh56e03.Y	77	29	CG534106	OST120799
267	13	44.8	77	14	CD941413	RBC_74 Ge	CD941413	RBC_74 Ge	77	29	CG534148	OST120852
268	13	44.8	77	29	CG509705	OST60991	CG509705	OST60991	77	29	CG534204	OST120919
269	13	44.8	78	9	AI754972	Arabidops	AI754972	Arabidops	77	29	CG558425	OST175926
270	13	44.8	78	9	AI458779	t174501.X	AI458779	t174501.X	78	28	AZ486464	IM0314D05
271	13	44.8	78	28	AZ437097	IM0225J08	AZ437097	IM0225J08	78	29	BX650431	Arabidops
272	13	44.8	78	29	AL941375	Arabidops	AL941375	Arabidops	79	9	AI611356	tu57H07.X
273	13	44.8	79	9	AI906717	QV-BT124-	AI906717	QV-BT124-	79	9	AU259915	AU259915
274	13	44.8	80	29	AL938071	Arabidops	AL938071	Arabidops	79	12	BG363804	dc71e03.Y
275	12.8	44.1	32	28	AZ583239	IM0378R08	AZ583239	IM0378R08	79	14	CF115782	SFP015D1
276	12.8	44.1	32	28	AZ766102	IM0563124	AZ766102	IM0563124	79	14	CF115782	SFP015D1
277	12.8	44.1	34	9	AI744308	tr09B07.X	AI744308	tr09B07.X	79	29	AL760717	Arabidops
278	12.8	44.1	34	12	BJ057665	BJ057665	BJ057665	BJ057665	80	9	AL776997	AL776997
279	12.8	44.1	36	28	BZ662586	SALK_0260	BZ662586	SALK_0260	80	12	BM114749	L0809F11-
280	12.8	44.1	37	9	AI802260	tj36007.X	AI802260	tj36007.X	80	28	BX357801	SALK_1312
281	12.8	44.1	41	29	CG772880	1123012E1	CG772880	1123012E1	80	28	BX357801	SALK_1312
282	12.8	44.1	43	9	AI669388	ty31H08.X	AI669388	ty31H08.X	80	28	BX661945	Arabidops
283	12.8	44.1	46	9	AI619428	ty38a03.X	AI619428	ty38a03.X	80	28	BX661945	Arabidops
284	12.8	44.1	49	9	AA727650	vu97607.r	AA727650	vu97607.r	80	28	AZ598587	IM0413A04
285	12.8	44.1	50	9	AU103614	AU103614	AU103614	AU103614	80	28	AZ598587	IM0413A04
286	12.8	44.1	50	9	AU103617	AU103617	AU103617	AU103617	80	28	AZ598587	IM0413A04
287	12.8	44.1	51	12	BG361927	GB46910.Y	BG361927	GB46910.Y	80	28	AZ598587	IM0413A04
288	12.8	44.1	52	14	CG683281	rj41f08.Y	CG683281	rj41f08.Y	80	28	AZ598587	IM0413A04
289	12.8	44.1	53	28	AZ920341	1006019D1	AZ920341	1006019D1	80	28	AZ598587	IM0413A04
290	12.8	44.1	54	28	BH857781	SALK_0873	BH857781	SALK_0873	80	28	AZ598587	IM0413A04
291	12.8	44.1	54	28	CC037327	3591.1.86	CC037327	3591.1.86	80	28	AZ598587	IM0413A04
292	12.8	44.1	57	14	CA777638	ip19502.Y	CA777638	ip19502.Y	80	28	AZ598587	IM0413A04
293	12.8	44.1	57	28	AZ433887	IM0220D01	AZ433887	IM0220D01	80	28	AZ598587	IM0413A04
294	12.8	44.1	58	29	CG362523	lem5088.1	CG362523	lem5088.1	80	28	AZ598587	IM0413A04
295	12.8	44.1	58	29	AL942674	Arabidops	AL942674	Arabidops	80	28	AZ598587	IM0413A04
296	12.8	44.1	60	9	AW004452	701931486	AW004452	701931486	80	28	AZ598587	IM0413A04

C 370	12.6	43.4	55	9	AI913058	AI913058 tz75f07.x	C 443	12.4	42.8	45	29	AG206278	Oryza sat
C 371	12.6	43.4	57	9	AU252594	AU252594	444	12.4	42.8	46	28	AZ833686	2M0115L20
C 372	12.6	43.4	57	13	BX553132	BX553132 BX553132	445	12.4	42.8	49	9	AA846570	aj97c02.s
C 373	12.6	43.4	57	28	BH484364	BH484364 SALK_0695	446	12.4	42.8	49	10	AW334086	S30C3 AGS
C 374	12.6	43.4	57	28	BH850801	BH850801 SALK_0718	447	12.4	42.8	49	14	CF321218	HD--12-G0
C 375	12.6	43.4	58	9	AU010373	AU010373	448	12.4	42.8	49	14	W86814	zb61f02.r1
C 376	12.6	43.4	58	14	CB274954	CB274954 ku73d01.y	449	12.4	42.8	50	29	AL945912	Arabiidops
C 377	12.6	43.4	58	28	BH904512	BH904512 SALK_1045	450	12.4	42.8	51	28	BH862718	CSRL-125312
C 378	12.6	43.4	61	9	AI650326	AI650326 wai8e08.x	451	12.4	42.8	52	9	AI540848	tp68c11.x
C 379	12.6	43.4	61	9	AA554915	AA554915 nk31e06.s	452	12.4	42.8	52	9	AI697308	AI697308 tq07f02.x
C 380	12.6	43.4	61	9	AA595454	AA595454 nk34d06.s	453	12.4	42.8	52	9	AU256791	AU256791
C 381	12.6	43.4	61	14	CF053677	CF053677 QCN1b04.y	454	12.4	42.8	53	9	AI224228	qx26e09.x
C 382	12.6	43.4	61	29	CS510250	CS510250 QST61872	455	12.4	42.8	53	13	BX562212	BX562212
C 383	12.6	43.4	62	9	AV365244	AV365244	456	12.4	42.8	54	28	BH910562	BH910562
C 384	12.6	43.4	62	29	CG615433	CG615433 OST305392	457	12.4	42.8	54	29	BX001821	BX001821
C 385	12.6	43.4	63	14	CD401366	CD401366 Gm CK2346	458	12.4	42.8	55	2	HSM001638	HSM001638
C 386	12.6	43.4	64	9	AI670974	AI670974 wbi2f03.x	459	12.4	42.8	55	9	AI913453	AI913453
C 387	12.6	43.4	64	9	AA594204	AA594204 nn39d04.s	460	12.4	42.8	55	9	BE321082	BE321082
C 388	12.6	43.4	64	14	CF017541	CF017541 OBM25e10.	461	12.4	42.8	55	29	AL760223	Arabiidops
C 389	12.6	43.4	65	12	BH898426	BH898426 p65e05.y	462	12.4	42.8	55	29	AL760223	Arabiidops
C 390	12.6	43.4	65	29	CS458761	CS458761 OBT146689	463	12.4	42.8	56	12	BI491371	df07h12.w
C 391	12.6	43.4	66	29	AG260513	AG260513 Lotus cor	464	12.4	42.8	56	12	BM445434	11L11C9.a
C 392	12.6	43.4	67	9	AA894821	AA894821 oj61d12.s	465	12.4	42.8	56	13	BQ787611	im13b12.x
C 393	12.6	43.4	67	9	AI917918	AI917918 tz14f06.x	466	12.4	42.8	56	29	AL943575	AL943575
C 394	12.6	43.4	67	13	BQ075738	BQ075738 f08c12.y	467	12.4	42.8	57	12	BG235467	BG235467
C 395	12.6	43.4	67	14	CB261630	CB261630 93-E8866-	468	12.4	42.8	57	28	AZ657854	1M0534L15
C 396	12.6	43.4	67	14	CD953649	CD953649 SBJ_4 Gen	469	12.4	42.8	57	28	AZ657854	1M0534L15
C 397	12.6	43.4	69	29	CNS025UP	AI182554 Tetradon	470	12.4	42.8	57	28	AZ782127	AZ782127
C 398	12.6	43.4	70	9	AA931825	AA931825 omb3a06.s	471	12.4	42.8	58	9	AI709231	at01f04.x
C 399	12.6	43.4	70	9	AL780467	AL780467 AL780467	472	12.4	42.8	58	28	AZ834846	AZ834846
C 400	12.6	43.4	70	14	CB359615	CB359615 ZF001-P00	473	12.4	42.8	58	28	BH789684	BH789684
C 401	12.6	43.4	71	12	BH898279	BH898279 ph62f08.y	474	12.4	42.8	60	9	AI539048	AI539048
C 402	12.6	43.4	71	28	AZ786367	AZ786367 2M0031016	475	12.4	42.8	60	9	AI719784	AI719784
C 403	12.6	43.4	71	29	CNS02ABD	AI188338 Tetradon	476	12.4	42.8	60	9	AU268022	AU268022
C 404	12.6	43.4	72	10	BH977483	BH977483 b654e10.y	477	12.4	42.8	60	9	AW020312	df07h12.y
C 405	12.6	43.4	73	12	BG621583	BG621583 602617180	478	12.4	42.8	60	29	CF793054	SALK_0074
C 406	12.6	43.4	73	14	CD960600	CD960600 SDE_274 G	479	12.4	42.8	63	14	CF806791	CF806791
C 407	12.6	43.4	73	29	CG529491	CG529491 OBT109956	480	12.4	42.8	63	28	BH415699	BH415699
C 408	12.6	43.4	73	29	CG664820	CG664820 OST452459	481	12.4	42.8	64	10	BE318333	BE318333
C 409	12.6	43.4	74	9	AL660462	AL660462 AL660462	482	12.4	42.8	64	10	BF118524	BF118524
C 410	12.6	43.4	74	28	B2357883	B2357883 SALK_1314	483	12.4	42.8	64	10	BF154369	BF154369
C 411	12.6	43.4	75	9	AI696772	AI696772 wc61d07.x	484	12.4	42.8	64	10	BF219632	BF219632
C 412	12.6	43.4	75	9	AA598953	AA598953 ae37h08.s	485	12.4	42.8	64	29	TA78H01P	TA78H01P
C 413	12.6	43.4	75	9	AA615120	AA615120 vno2b09.r	486	12.4	42.8	65	28	BH908271	BH908271
C 414	12.6	43.4	75	10	BH223726	BH223726 kp88a10.y	487	12.4	42.8	65	29	FR0053439	FR0053439
C 415	12.6	43.4	75	28	BH910959	BH910959 SALK_0636	488	12.4	42.8	65	29	BX659554	BX659554
C 416	12.6	43.4	75	28	CC179654	CC179654 SALK_0719	489	12.4	42.8	65	29	AA884345	AA884345
C 417	12.6	43.4	75	29	CS520478	CS520478 CH240_367	490	12.4	42.8	66	12	BG361618	BG361618
C 418	12.6	43.4	75	29	AG218208	AG218208 Drosophila	491	12.4	42.8	66	12	CF115732	CF115732
C 419	12.6	43.4	76	9	AI316047	AI316047 uj61g05.y	492	12.4	42.8	66	14	CF115732	CF115732
C 420	12.6	43.4	76	9	AU011284	AU011284 AU011284	493	12.4	42.8	66	28	AZ787829	AZ787829
C 421	12.6	43.4	76	28	BZ289518	BZ289518 SALK_0229	494	12.4	42.8	66	29	AG646385	AG646385
C 422	12.6	43.4	76	29	CG475280	CG475280 OST3535 M	495	12.4	42.8	67	9	AA659476	AA659476
C 423	12.6	43.4	77	14	CB263298	CB263298 66-E9721-	496	12.4	42.8	67	9	AI912173	AI912173
C 424	12.6	43.4	77	14	R38641	R38641 vt59b10.r1	497	12.4	42.8	67	9	AI921937	AI921937
C 425	12.6	43.4	77	29	CG899207	CG899207 01S0620-0	498	12.4	42.8	68	13	BX708928	BX708928
C 426	12.6	43.4	78	9	AA334074	AA334074 on78d07.s	499	12.4	42.8	69	29	AI950439	AI950439
C 427	12.6	43.4	78	28	BH904967	BH904967 SALK_1054	500	12.4	42.8	69	29	AI650934	AI650934
C 428	12.6	43.4	79	29	AL951473	AL951473 Arabidops	501	12.4	42.8	70	14	CB935228	CB935228
C 429	12.6	43.4	80	29	BX662420	BX662420 Arabidops	502	12.4	42.8	70	28	BH850759	BH850759
C 430	12.4	42.8	80	28	BH790181	BH790181 SALK_0565	503	12.4	42.8	70	28	CG759791	CG759791
C 431	12.4	42.8	80	28	AZ416940	AZ416940 1M0192H21	504	12.4	42.8	71	13	BQ692851	BQ692851
C 432	12.4	42.8	80	28	AU759110	AU759110 AU759110	505	12.4	42.8	71	13	BQ693463	BQ693463
C 433	12.4	42.8	80	28	BF032106	BF032106 601559696	506	12.4	42.8	71	13	BQ693466	BQ693466
C 434	12.4	42.8	80	14	CF032899	CF032899 7LEAF--08	507	12.4	42.8	71	14	X98200	X98200
C 435	12.4	42.8	80	9	AU011968	AU011968 AU011968	508	12.4	42.8	71	28	BH789678	BH789678
C 436	12.4	42.8	80	9	AU011969	AU011969 AU011969	509	12.4	42.8	71	28	BH789678	BH789678
C 437	12.4	42.8	80	9	AU011971	AU011971 AU011971	510	12.4	42.8	71	29	CG545852	CG545852
C 438	12.4	42.8	80	9	AU011973	AU011973 AU011973	511	12.4	42.8	71	29	CG545852	CG545852
C 439	12.4	42.8	80	28	BH852384	BH852384 SALK_0745	512	12.4	42.8	71	29	CG545852	CG545852
C 440	12.4	42.8	80	28	BZ352392	BZ352392 SALK_0789	513	12.4	42.8	71	29	CG545852	CG545852
C 441	12.4	42.8	80	28	BX659541	BX659541 Arabidops	514	12.4	42.8	73	10	BF123392	BF123392
C 442	12.4	42.8	80	28	BH808431	BH808431 100807991	515	12.4	42.8	73	14	CD866433	CD866433

516	12.4	42.8	73	14	U44288	U44288	ENU44288 AS	C 589	12.2	42.1	58	9	AV739274	AV739274	AV739274	AV739274
517	12.4	42.8	74	9	AI379808	AI379808	tb91c04.x	C 590	12.2	42.1	58	9	AA506617	AA506617	AA506617	AA506617
518	12.4	42.8	74	14	CF651628	CF651628	10-102016	C 591	12.2	42.1	58	14	AZ499503	AZ499503	IM0337M13	IM0337M13
519	12.4	42.8	75	9	AI307206	AI307206	tb36h07.x	C 592	12.2	42.1	59	28	CF881253	CF881253	trlc026xm	trlc026xm
520	12.4	42.8	75	12	BI703772	BI703772	xx20912.y	C 593	12.2	42.1	59	28	BZ595463	BZ595463	SALK 0870	SALK 0870
521	12.4	42.8	75	12	BM571633	BM571633	fx04a07.x	C 594	12.2	42.1	59	28	BZ595463	BZ595463	SALK 0870	SALK 0870
522	12.4	42.8	75	28	AZ398065	AZ398065	IM0163M17	C 595	12.2	42.1	61	9	AI440824	AI440824	sa8e611.y	sa8e611.y
523	12.4	42.8	75	28	AZ785373	AZ785373	2M0029A13	C 596	12.2	42.1	61	13	BQ479345	BQ479345	ku3jd12.y	ku3jd12.y
524	12.4	42.8	76	9	AA741550	AA741550	0B29040.s	C 597	12.2	42.1	61	28	BZ289575	BZ289575	SALK 0229	SALK 0229
525	12.4	42.8	76	9	AI633915	AI633915	tt23a07.x	C 598	12.2	42.1	61	29	CG666107	CG666107	OST455751	OST455751
526	12.4	42.8	76	9	AW059618	AW059618	HUTH.bsst	C 599	12.2	42.1	62	9	AA026245	AA026245	zj99a02.s	zj99a02.s
527	12.4	42.8	76	28	BZ596072	BZ596072	SALK_0920	C 600	12.2	42.1	62	9	AI481932	AI481932	vh86d11.x	vh86d11.x
528	12.4	42.8	76	28	BZ596073	BZ596073	SALK_0920	C 601	12.2	42.1	62	9	AI481932	AI481932	vh86d11.x	vh86d11.x
529	12.4	42.8	76	28	AI945898	AI945898	ArabiIdops	C 602	12.2	42.1	62	29	EX165948	EX165948	Danio rer	Danio rer
530	12.4	42.8	77	10	AW516108	AW516108	xt60h07.x	C 603	12.2	42.1	63	12	EG361068	EG361068	gb45e09.y	gb45e09.y
531	12.4	42.8	78	9	AA936218	AA936218	on43c10.x	C 604	12.2	42.1	63	28	BZ597224	BZ597224	SALK_1005	SALK_1005
532	12.4	42.8	78	9	AI252514	AI252514	qv30c11.x	C 605	12.2	42.1	64	9	AI570111	AI570111	tr74d11.x	tr74d11.x
533	12.4	42.8	79	9	AA144854	AA144854	mi73c08.x	C 606	12.2	42.1	64	9	AL662232	AL662232	AL662232	AL662232
534	12.4	42.8	79	29	AI943953	AI943953	ArabiIdops	C 607	12.2	42.1	64	9	AA594319	AA594319	nl92h02.s	nl92h02.s
535	12.2	42.1	31	28	AZ997553	AZ997553	2M0284E10	C 608	12.2	42.1	64	10	AA409544	AA409544	SWOV3WCAM	SWOV3WCAM
536	12.2	42.1	33	28	BH740759	BH740759	KG01661-3	C 609	12.2	42.1	64	10	BB638296	BB638296	SNOWMFCAR	SNOWMFCAR
537	12.2	42.1	33	28	BH791695	BH791695	SALK_0608	C 610	12.2	42.1	64	10	BF118530	BF118530	SWOV13CAN	SWOV13CAN
538	12.2	42.1	37	28	AZ376645	AZ376645	IM0130A08	C 611	12.2	42.1	64	12	EG092541	EG092541	mac12h03.	mac12h03.
539	12.2	42.1	38	29	DME545254	DME545254	KG03386-5	C 612	12.2	42.1	64	14	CD397787	CD397787	Gm ck1872	Gm ck1872
540	12.2	42.1	39	28	BH840522	BH840522	KG03386-5	C 613	12.2	42.1	64	14	D20622	D20622	HUMG301597	HUMG301597
541	12.2	42.1	40	13	CO0969	CO0969	HUMG3000333	C 614	12.2	42.1	64	28	AZ775161	AZ775161	2M0007P15	2M0007P15
542	12.2	42.1	40	28	AZ815739	AZ815739	2M0084K13	C 615	12.2	42.1	64	28	BH811901	BH811901	SALK_0604	SALK_0604
543	12.2	42.1	42	9	AI833018	AI833018	at74c04.x	C 616	12.2	42.1	64	29	CG629148	CG629148	OST340948	OST340948
544	12.2	42.1	43	9	AI758314	AI758314	ty06c01.x	C 617	12.2	42.1	64	29	EX291457	EX291457	ArabiIdops	ArabiIdops
545	12.2	42.1	43	29	AL766396	AL766396	ArabiIdops	C 618	12.2	42.1	64	29	TA121E03P	TA121E03P	T. brucei	T. brucei
546	12.2	42.1	44	29	BX121347	BX121347	Danio rer	C 619	12.2	42.1	64	29	AA208741	AA208741	mu65d06.r	mu65d06.r
547	12.2	42.1	45	28	BH853902	BH853902	SALK_0784	C 620	12.2	42.1	65	9	AA208741	AA208741	mu65d06.r	mu65d06.r
548	12.2	42.1	46	9	AI624478	AI624478	tb68e05.x	C 621	12.2	42.1	65	10	AA23329	AA23329	sh66c03.y	sh66c03.y
549	12.2	42.1	46	28	BH792322	BH792322	SALK_0634	C 622	12.2	42.1	65	10	AD943273	AD943273	RCN_128.G	RCN_128.G
550	12.2	42.1	47	29	AL756982	AL756982	ArabiIdops	C 623	12.2	42.1	65	14	CD943324	CD943324	RCO_26.Ge	RCO_26.Ge
551	12.2	42.1	47	29	TA92D04Q	TA92D04Q	T. brucei	C 624	12.2	42.1	65	14	CF298453	CF298453	7LRAF-01	7LRAF-01
552	12.2	42.1	48	28	BH901374	BH901374	SALK_0786	C 625	12.2	42.1	65	28	AZ330554	AZ330554	IM0058A01	IM0058A01
553	12.2	42.1	49	9	AV960827	AV960827	AV960827	C 626	12.2	42.1	65	28	BZ381976	BZ381976	SALK_1176	SALK_1176
554	12.2	42.1	49	12	BI840176	BI840176	se70e02.y	C 627	12.2	42.1	65	29	CG566789	CG566789	OST193684	OST193684
555	12.2	42.1	49	13	BQ613516	BQ613516	rd08e10.y	C 628	12.2	42.1	65	29	CG785992	CG785992	98F0079-0	98F0079-0
556	12.2	42.1	49	29	BX649704	BX649704	ArabiIdops	C 629	12.2	42.1	66	9	AI571487	AI571487	tr55610.x	tr55610.x
557	12.2	42.1	49	29	BX893214	BX893214	ArabiIdops	C 630	12.2	42.1	66	9	AI906226	AI906226	CM-BT106-	CM-BT106-
558	12.2	42.1	50	13	C92347	C92347	Dict	C 631	12.2	42.1	66	28	AZ623479	AZ623479	IM0461116	IM0461116
559	12.2	42.1	51	12	BG272969	BG272969	nai56g11.	C 632	12.2	42.1	66	28	CG556234	CG556234	OST171625	OST171625
560	12.2	42.1	51	28	AZ836163	AZ836163	2M0130E20	C 633	12.2	42.1	66	29	CG570250	CG570250	OST198988	OST198988
561	12.2	42.1	51	28	AL755958	AL755958	ArabiIdops	C 634	12.2	42.1	66	29	TA127H04P	TA127H04P	T. brucei	T. brucei
562	12.2	42.1	51	29	BX126671	BX126671	Danio rer	C 635	12.2	42.1	67	9	AI708576	AI708576	sb98f04.x	sb98f04.x
563	12.2	42.1	51	29	BX241836	BX241836	Danio rer	C 636	12.2	42.1	67	9	AI930923	AI930923	sb44f10.y	sb44f10.y
564	12.2	42.1	51	29	DME545740	DME545740	Drosophila	C 637	12.2	42.1	67	9	AI936499	AI936499	wd28f07.x	wd28f07.x
565	12.2	42.1	52	9	AI371545	AI371545	ta51a02.x	C 638	12.2	42.1	67	14	CD946435	CD946435	REN_47.Ge	REN_47.Ge
566	12.2	42.1	52	14	CD571135	CD571135	kb72e09.y	C 639	12.2	42.1	67	14	CD966066	CD966066	SEL_513.G	SEL_513.G
567	12.2	42.1	52	28	B00225	B00225	CSRL-104f2-	C 640	12.2	42.1	67	28	BH909420	BH909420	SALK_0535	SALK_0535
568	12.2	42.1	52	28	BH27683	BH27683	100614180	C 641	12.2	42.1	68	9	AI880472	AI880472	at78c12.x	at78c12.x
569	12.2	42.1	53	9	AA523590	AA523590	sa27f03.	C 642	12.2	42.1	68	10	BF144216	BF144216	601786828	601786828
570	12.2	42.1	53	12	BM891460	BM891460	sa27f03.	C 643	12.2	42.1	68	10	BF144216	BF144216	601786828	601786828
571	12.2	42.1	53	28	BZ222235	BZ222235	SALK_1236	C 644	12.2	42.1	69	10	AW543368	AW543368	CO169A10-	CO169A10-
572	12.2	42.1	53	29	AL940874	AL940874	ArabiIdops	C 645	12.2	42.1	69	10	AW543368	AW543368	CO169A10-	CO169A10-
573	12.2	42.1	54	10	BF643243	BF643243	NF003A01E	C 646	12.2	42.1	69	14	R05841	R05841	ye88e09.t1	ye88e09.t1
574	12.2	42.1	54	12	BG408955	BG408955	gb84c06.y	C 647	12.2	42.1	69	28	BH852849	BH852849	SALK_0756	SALK_0756
575	12.2	42.1	54	28	BH234921	BH234921	MHAA_C04	C 648	12.2	42.1	69	29	CNS02XR5	CNS02XR5	Tetraodon	Tetraodon
576	12.2	42.1	54	29	AL764743	AL764743	ArabiIdops	C 649	12.2	42.1	70	13	BQ480126	BQ480126	faa86d04.	faa86d04.
577	12.2	42.1	55	12	BM068726	BM068726	te84b02.y	C 650	12.2	42.1	70	13	BUS76112	BUS76112	TgsSTzyD8	TgsSTzyD8
578	12.2	42.1	55	28	AZ339859	AZ339859	IM0071F02	C 651	12.2	42.1	70	14	CF051215	CF051215	QCM22F12.	QCM22F12.
579	12.2	42.1	55	28	AZ339859	AZ339859	IM0071F02	C 652	12.2	42.1	70	28	AZ649694	AZ649694	IM0519N24	IM0519N24
580	12.2	42.1	56	13	C21299	C21299	HUMG3000237	C 653	12.2	42.1	70	28	AZ649694	AZ649694	IM0519N24	IM0519N24
581	12.2	42.1	56	28	AZ332343	AZ332343	IM0044F06	C 654	12.2	42.1	70	28	BH759592	BH759592	KG05236-3	KG05236-3
582	12.2	42.1	56	28	B00285	B00285	CSRL-106a12	C 655	12.2	42.1	71	9	AA711146	AA711146	vt55602.r	vt55602.r
583	12.2	42.1	57	14	CB921893	CB921893	VVD076H05	C 656	12.2	42.1	71	13	C20932	C20932	HUMG3000220	HUMG3000220
584	12.2	42.1	57	14	CD345677	CD345677	ECEsteF96	C 657	12.2	42.1	71	14	CB263121	CB263121	33-B9777-	33-B9777-
585	12.2	42.1	57	28	AZ992314	AZ992314	2M0276K23	C 658	12.2	42.1	72	28	AZ401745	AZ401745	IM0168K10	IM0168K10
586	12.2	42.1	57	28	B03449	B03449	CSRL-179G3-	C 659	12.2	42.1	72	28	AZ782821	AZ782821	2M0024G05	2M0024G05
587	12.2	42.1	58	9	AI016152	AI016152	ot73e02.s	C 660	12.2	42.1	72	28	BZ596806	BZ596806	SALK_0360	SALK_0360
588	12.2	42.1	58	9	AI965857	AI965857	sc78g02.y	C 661	12.2	42.1	72	28	BZ661345	BZ661345	SALK_0248	SALK_0248

662	12.2	42.1	72	28	BZ769841	BZ769841 SALK_1427	C 735	12	41.4	52	9	AI801812	AI801812 to95g10.x
663	12.2	42.1	73	9	AI330688	AI330688 fa91g03.y	C 736	12	41.4	52	14	T85359	T85359 y082d08.s1
664	12.2	42.1	73	10	BZ228733	BZ228733 SMOVL3CAN	C 737	12	41.4	52	28	AZ843322	AZ843322 2M0142G09
665	12.2	42.1	73	12	BI107307	BI107307 602894328	C 738	12	41.4	52	29	AB081935	AB081935 Drosophil
666	12.2	42.1	73	29	AI771410	AI771410 Arabidops	C 739	12	41.4	52	29	TA121B12Q	TA121B12Q T. brucei
667	12.2	42.1	74	13	BQ275575	BQ275575 D336f10.y	C 740	12	41.4	53	9	AL790756	AL790756 AL790756
668	12.2	42.1	74	14	CD913649	CD913649 G608.114B	C 741	12	41.4	53	28	B01982	B01982 CSRL-144H11
669	12.2	42.1	74	29	AI767013	AI767013 Arabidops	C 742	12	41.4	54	28	AZ866258	AZ866258 2M0176M08
670	12.2	42.1	75	9	AI938927	AI938927 sc63a02.y	C 743	12	41.4	54	28	CF384789	CF384789 caa11c04.
671	12.2	42.1	75	13	BH787450	BH787450 V047D08.P	C 744	12	41.4	55	28	BH908756	BH908756 SALK_0504
672	12.2	42.1	75	14	CK098783	CK098783 A031P73.5	C 745	12	41.4	56	9	AL695651	AL695651 AL695651
673	12.2	42.1	75	28	BH408587	BH408587 1007005C0	C 746	12	41.4	56	28	AZ424951	AZ424951 1M0204KL5
674	12.2	42.1	75	28	BH911917	BH911917 SALK_0730	C 747	12	41.4	56	29	CG799256	CG799256 1118001B0
675	12.2	42.1	75	29	CG475700	CG475700 OS*4213.M	C 748	12	41.4	56	29	AL762058	AL762058 Arabidops
676	12.2	42.1	76	29	CG706108	CG706108 0150707-0	C 749	12	41.4	57	13	BX778267	BX778267 BX778267
677	12.2	42.1	76	9	AA502239	AA502239 ne94d05.s	C 750	12	41.4	58	9	AI584456	AI584456 fb93h12.x
678	12.2	42.1	76	10	AW194637	AW194637 xn42g04.x	C 751	12	41.4	58	13	BQ524737	BQ524737 NISC no06
679	12.2	42.1	76	10	BZ867849	BZ867849 601443622	C 752	12	41.4	59	14	CB305221	CB305221 3*EST-NFL
680	12.2	42.1	76	28	AQ025263	AQ025263 EP(3) 3081	C 753	12	41.4	59	28	BZ292774	BZ292774 SALK_1283
681	12.2	42.1	76	28	BZ380384	BZ380384 SALK_1150	C 754	12	41.4	60	9	AI949039	AI949039 wg36c03.x
682	12.2	42.1	76	29	CG659835	CG659835 OS*435402	C 755	12	41.4	60	10	BF651039	BF651039 NF109H0E
683	12.2	42.1	76	29	CG706108	CG706108 0150707-0	C 756	12	41.4	60	14	CB410162	CB410162 NISC nc09
684	12.2	42.1	77	9	AL866175	AL866175 Arabidops	C 757	12	41.4	60	29	BX661937	BX661937 Arabidops
685	12.2	42.1	77	9	AL866175	AL866175 Arabidops	C 758	12	41.4	61	9	AI000397	AI000397 ot06e12.s
686	12.2	42.1	77	10	AW700694	AW700694 pa43b07.y	C 759	12	41.4	61	9	AU007077	AU007077 AU007077
687	12.2	42.1	77	28	AF067770	AF067770 AF067770	C 760	12	41.4	61	28	BH863498	BH863498 SALK_0940
688	12.2	42.1	77	28	AZ982711	AZ982711 2M0263C07	C 761	12	41.4	61	29	CG568127	CG568127 OT194882
689	12.2	42.1	77	29	CG479385	CG479385 OS*10166	C 762	12	41.4	61	29	TA337H01Q	TA337H01Q T. brucei
690	12.2	42.1	77	29	CG610667	CG610667 OS*294349	C 763	12	41.4	62	29	CG475777	CG475777 Arabidops
691	12.2	42.1	77	29	AL763184	AL763184 Arabidops	C 764	12	41.4	62	29	AL756677	AL756677 Arabidops
692	12.2	42.1	78	9	AL854995	AL854995 Arabidops	C 765	12	41.4	63	29	CG475498	CG475498 OST3832.M
693	12.2	42.1	78	10	BF438294	BF438294 7q07e06.x	C 766	12	41.4	63	29	CG600185	CG600185 OST268992
694	12.2	42.1	78	13	BQ244462	BQ244462 TaEL15037B	C 767	12	41.4	64	10	BE318106	BE318106 SF026H0BL
695	12.2	42.1	78	28	BH810230	BH810230 SALK_0482	C 768	12	41.4	64	10	BE318106	BE318106 SF026H0BL
696	12.2	42.1	78	29	AG260396	AG260396 Letuvs cor	C 769	12	41.4	64	14	CA819198	CA819198 sau70f08.
697	12.2	42.1	79	9	AV970178	AV970178 AV970178	C 770	12	41.4	64	14	CA819198	CA819198 sau70f08.
698	12.2	42.1	79	9	AA536213	AA536213 nj83d01.s	C 771	12	41.4	65	12	BM282506	BM282506 k127803.y
699	12.2	42.1	79	14	CA942759	CA942759 ir67a01.x	C 772	12	41.4	65	12	BM282506	BM282506 k127803.y
700	12.2	42.1	79	14	CG099478	CG099478 A069P50.5	C 773	12	41.4	66	9	AL875574	AL875574 k180g07.y
701	12.2	42.1	79	14	TS9637	TS9637 ycl3c10.s1	C 774	12	41.4	66	9	AI567096	AI567096 tq85b07.x
702	12.2	42.1	80	9	AL932289	AL932289 AL932289	C 775	12	41.4	66	9	AL875574	AL875574 k180g07.y
703	12.2	42.1	80	12	BM131658	BM131658 TGESTZyA7	C 776	12	41.4	66	9	AU259021	AU259021 AU259021
704	12.2	42.1	80	13	BUT90880	BUT90880 TGESTZyB5	C 777	12	41.4	66	12	BJ079690	BJ079690 BJ079690
705	12.2	42.1	80	14	CB368403	CB368403 TGESTZyH0	C 778	12	41.4	66	12	CF115732	CF115732 SSF08E18
706	12.2	42.1	80	14	CB831912	CB831912 NCERT3A56	C 779	12	41.4	66	14	CF115732	CF115732 SSF08E18
707	12.2	42.1	80	14	CF043983	CF043983 QCU23909.	C 780	12	41.4	66	28	AZ404471	AZ404471 1M0172B16
708	12.2	42.1	80	14	CF319668	CF319668 HD--10-E0	C 781	12	41.4	66	28	AZ404471	AZ404471 1M0172B16
709	12.2	42.1	80	14	N36623	N36623 Yx88d04.r1	C 782	12	41.4	66	28	BH631033	BH631033 1007096C0
710	12.2	42.1	80	28	AZ781019	AZ781019 2M0018E24	C 783	12	41.4	66	28	BH631033	BH631033 1007096C0
711	12.2	42.1	80	28	CC182724	CC182724 XH802.Bay	C 784	12	41.4	66	28	BH631033	BH631033 1007096C0
712	12.2	42.1	80	29	CG481555	CG481555 OST14085	C 785	12	41.4	66	28	BH631033	BH631033 1007096C0
713	12.2	42.1	80	29	CG574141	CG574141 OST206705	C 786	12	41.4	66	28	BH631033	BH631033 1007096C0
714	12.2	42.1	80	29	AI646712	AI646712 ub64h07.x	C 787	12	41.4	66	28	BH631033	BH631033 1007096C0
715	12.2	42.1	80	29	AZ759923	AZ759923 1M0553110	C 788	12	41.4	66	28	BH631033	BH631033 1007096C0
716	12.2	42.1	80	29	AZ780490	AZ780490 2M0017G24	C 789	12	41.4	66	28	BH631033	BH631033 1007096C0
717	12.2	42.1	80	29	AJ546358	AJ546358 Drosophil	C 790	12	41.4	66	28	BH631033	BH631033 1007096C0
718	12.2	42.1	80	29	BH850881	BH850881 SALK_0720	C 791	12	41.4	66	28	BH631033	BH631033 1007096C0
719	12.2	42.1	80	29	AI913033	AI913033 tz75d02.x	C 792	12	41.4	66	28	BH631033	BH631033 1007096C0
720	12.2	42.1	80	29	AZ450474	AZ450474 1M0249A13	C 793	12	41.4	66	28	BH631033	BH631033 1007096C0
721	12.2	42.1	80	29	CC057354	CC057354 SALK_1406	C 794	12	41.4	66	28	BH631033	BH631033 1007096C0
722	12.2	42.1	80	29	AA975071	AA975071 on03d07.s	C 795	12	41.4	66	28	BH631033	BH631033 1007096C0
723	12.2	42.1	80	29	AI738832	AI738832 tz28g06.x	C 796	12	41.4	66	28	BH631033	BH631033 1007096C0
724	12.2	42.1	80	29	AU266053	AU266053 AU266053	C 797	12	41.4	66	28	BH631033	BH631033 1007096C0
725	12.2	42.1	80	29	AL771654	AL771654 Arabidops	C 798	12	41.4	66	28	BH631033	BH631033 1007096C0
726	12.2	42.1	80	29	BH910024	BH910024 SALK_0572	C 799	12	41.4	66	28	BH631033	BH631033 1007096C0
727	12.2	42.1	80	29	BZ765916	BZ765916 SALK_1355	C 800	12	41.4	66	28	BH631033	BH631033 1007096C0
728	12.2	42.1	80	29	AU104264	AU104264 AU104264	C 801	12	41.4	66	28	BH631033	BH631033 1007096C0
729	12.2	42.1	80	29	AU107304	AU107304 AU107304	C 802	12	41.4	66	28	BH631033	BH631033 1007096C0
730	12.2	42.1	80	29	BQ370398	BQ370398 nai33a04.	C 803	12	41.4	66	28	BH631033	BH631033 1007096C0
731	12.2	42.1	80	29	AQ026078	AQ026078 l(2)k1440	C 804	12	41.4	66	28	BH631033	BH631033 1007096C0
732	12.2	42.1	80	29	AZ774278	AZ774278 2M0003B04	C 805	12	41.4	66	28	BH631033	BH631033 1007096C0
733	12.2	42.1	80	29	B02642	B02642 CSRL-157H11	C 806	12	41.4	66	28	BH631033	BH631033 1007096C0
734	12.2	42.1	80	29	AA683922	AA683922 V794G03.f	C 807	12	41.4	66	28	BH631033	BH631033 1007096C0

C 808	12	41.4	70	28	BZ768793	SALK_1407	C 881	11.8	40.7	37	9	AU254992
C 809	12	41.4	28	BZ768795	SALK_1407	C 882	11.8	40.7	37	28	BZ378465	
C 810	12	41.4	70	29	CG494811	OST33882	883	11.8	40.7	39	12	BJ060351
C 811	12	41.4	71	9	AS562018	v12ln03.r	884	11.8	40.7	39	13	BX551703
C 812	12	41.4	71	14	CD943518	RCR_6 Gen	885	11.8	40.7	39	14	CF308197
C 813	12	41.4	71	14	CD945556	REA_26 Ge	886	11.8	40.7	39	14	H55495
C 814	12	41.4	71	14	CD964090	SDZ_22 Ge	C 887	11.8	40.7	40	9	A1918475
C 815	12	41.4	71	14	CF973311	PSU_bittr	C 888	11.8	40.7	40	12	BJ076521
C 816	12	41.4	71	28	BH846325	SALK_0072	C 889	11.8	40.7	40	13	BX554624
C 817	12	41.4	72	12	BI494677	df112a06	C 890	11.8	40.7	41	14	D18703
C 818	12	41.4	72	28	AZ489471	IM0321G23	C 891	11.8	40.7	41	14	H95705
C 819	12	41.4	72	28	CG541687	OST135165	C 892	11.8	40.7	41	28	AZ828170
C 820	12	41.4	73	12	BG310485	SMO33MCAM	C 893	11.8	40.7	42	14	CF291602
C 821	12	41.4	73	28	BZ661908	SALK_0253	C 894	11.8	40.7	42	28	BZ356968
C 822	12	41.4	73	29	AL944547	ArabiIdops	C 895	11.8	40.7	43	12	BJ078302
C 823	12	41.4	73	29	BX653912	ArabiIdops	C 896	11.8	40.7	46	9	AA131380
C 824	12	41.4	73	29	BX653912	ArabiIdops	C 897	11.8	40.7	46	28	BH910366
C 825	12	41.4	74	29	TA57C05P	ArabiIdops	C 898	11.8	40.7	47	28	BH910366
C 826	12	41.4	75	9	AW733972	v21h10.r	C 899	11.8	40.7	47	28	BH620060
C 827	12	41.4	75	28	BH855879	SALK_0844	C 900	11.8	40.7	47	28	BH910648
C 828	12	41.4	75	28	BH855886	SALK_0844	C 901	11.8	40.7	47	28	BH910817
C 829	12	41.4	75	29	CG490059	OST11622	C 902	11.8	40.7	48	29	EX187283
C 830	12	41.4	75	29	AL767314	ArabiIdops	C 903	11.8	40.7	49	9	AA411241
C 831	12	41.4	76	9	AW760638	n216C01.s	C 904	11.8	40.7	49	9	AA446096
C 832	12	41.4	76	13	BQ240244	TA805020B	C 905	11.8	40.7	49	10	BQ054816
C 833	12	41.4	76	14	CF298410	7LEAF--01	C 906	11.8	40.7	49	13	CA033671
C 834	12	41.4	76	28	BZ289798	SALK_0232	C 907	11.8	40.7	49	28	BH911354
C 835	12	41.4	76	29	CG616155	OST307956	C 908	11.8	40.7	49	28	CC049611
C 836	12	41.4	77	9	AL669640	tw34909.x	C 909	11.8	40.7	49	29	PCB303697
C 837	12	41.4	77	9	AL897168	AL897168	C 910	11.8	40.7	50	9	AI241767
C 838	12	41.4	77	9	AW025775	wu07G03.x	C 911	11.8	40.7	50	9	AU255886
C 839	12	41.4	77	14	CK137902	ma198h02.	C 912	11.8	40.7	50	14	CF291606
C 840	12	41.4	77	28	BH846367	SALK_0074	C 913	11.8	40.7	50	29	AL766868
C 841	12	41.4	77	29	AL759596	ArabiIdops	C 914	11.8	40.7	51	12	BM897715
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C 845	12	41.4	78	29	AL953578	ArabiIdops	C 918	11.8	40.7	52	9	AI702024
C 846	12	41.4	79	9	AW025781	ok72C09.s	C 919	11.8	40.7	52	9	AA165996
C 847	12	41.4	79	9	AS37245	tp01f03.x	C 920	11.8	40.7	52	10	BQ632167
C 848	12	41.4	79	9	AU260306	AU260306	C 921	11.8	40.7	52	10	AM695612
C 849	12	41.4	79	12	BI941858	gd56b11.y	C 922	11.8	40.7	52	14	CB263582
C 850	12	41.4	79	14	CB264027	95-E01502	C 923	11.8	40.7	52	14	CB295562
C 851	12	41.4	79	14	CB272642	ma160h05.	C 924	11.8	40.7	52	28	BQ3257
C 852	12	41.4	79	14	CF249356	1472b03.y	C 925	11.8	40.7	52	29	CG730209
C 853	12	41.4	79	28	AZ767575	1W0566017	C 926	11.8	40.7	53	9	AI591010
C 854	12	41.4	79	28	BZ356601	SALK_1293	C 927	11.8	40.7	53	10	AM251017
C 855	12	41.4	79	28	BZ356672	SALK_1296	C 928	11.8	40.7	54	9	AU013371
C 856	12	41.4	79	29	AL941184	ArabiIdops	C 929	11.8	40.7	54	9	AU013427
C 857	12	41.4	80	9	AL7424092	tf42901.x	C 930	11.8	40.7	54	9	AU013694
C 858	12	41.4	80	14	CF331598	NACL--07-	C 931	11.8	40.7	54	14	CB914552
C 859	12	41.4	80	14	CF331599	NACL--07-	C 932	11.8	40.7	54	28	BH096666
C 860	12	41.4	80	28	AZ508753	IM0351B24	C 933	11.8	40.7	55	28	BH096666
C 861	12	41.4	80	28	AZ771588	IM0574G06	C 934	11.8	40.7	55	28	BH814055
C 862	12	41.4	80	29	CG546048	OST145001	C 935	11.8	40.7	56	28	AZ318460
C 863	12	41.4	80	29	CG549290	OST152453	C 936	11.8	40.7	56	28	BZ770420
C 864	12	41.4	80	29	CG595136	OST254099	C 937	11.8	40.7	56	29	AL763067
C 865	12	41.4	80	29	CG615969	OST307488	C 938	11.8	40.7	56	29	AL942742
C 866	11.8	40.7	24	28	BH853176	SALK_0761	C 939	11.8	40.7	57	9	AU255578
C 867	11.8	40.7	26	28	AZ594424	IM0403A20	C 940	11.8	40.7	57	10	BF718323
C 868	11.8	40.7	27	28	BH857744	SALK_0157	C 941	11.8	40.7	57	10	BF054916
C 869	11.8	40.7	27	29	CG723079	1119074F0	C 942	11.8	40.7	57	28	BQ3111
C 870	11.8	40.7	29	28	AZ771246	IM0573G18	C 943	11.8	40.7	57	28	CG326470
C 871	11.8	40.7	30	28	AZ345702	IM0080G03	C 944	11.8	40.7	57	29	CG731292
C 872	11.8	40.7	33	28	AZ445462	IM0241K14	C 945	11.8	40.7	58	9	AI246109
C 873	11.8	40.7	34	9	AA915753	v235b08.r	C 946	11.8	40.7	58	9	AI367559
C 874	11.8	40.7	34	9	AI378501	tc56h07.x	C 947	11.8	40.7	58	9	AI178732
C 875	11.8	40.7	34	28	BH846289	SALK_0071	C 948	11.8	40.7	58	9	AI179529
C 876	11.8	40.7	34	28	BH861864	SALK_0881	C 949	11.8	40.7	58	14	CA850023
C 877	11.8	40.7	35	28	BH906541	SALK_0338	C 950	11.8	40.7	58	28	BH70391
C 878	11.8	40.7	35	29	AG228557	Lotus cor	C 951	11.8	40.7	58	29	BX654856
C 879	11.8	40.7	35	29	AL765859	ArabiIdops	C 952	11.8	40.7	59	13	BQ582890
C 880	11.8	40.7	36	10	AW249790	2819641.3	C 953	11.8	40.7	59	14	CB258816

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955      11.8      40.7      59 29 BX658971 BX658971 Arabidops
956      11.8      40.7      60 14 CD920418 CD920418 G608.117A
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960      11.8      40.7      61 9   AI284354 AI284354 g170g05.x
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972      11.8      40.7      62 12 BG272655 BG272655 nah35a07
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977      11.8      40.7      62 29 AL762490 AL762490 Arabidops
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981      11.8      40.7      63 14 CA337118 CA337118 NISC lv09
982      11.8      40.7      63 28 AZ871148 AZ871148 2M018321
983      11.8      40.7      63 28 BH910796 BH910796 SALK 0826
984      11.8      40.7      63 28 CG459412 CG459412 SALK 1281
985      11.8      40.7      63 29 CG579755 CG579755 OST218442
986      11.8      40.7      64 9   AI139686 AI139686 qc20d09.x
987      11.8      40.7      64 9   AI247119 AI247119 gx52f10.x
988      11.8      40.7      64 9   AI522566 AI522566 fb59d04.x
989      11.8      40.7      64 9   AI627636 AI627636 ey18g08.x
990      11.8      40.7      64 9   AA595043 AA595043 md40e11.s
991      11.8      40.7      64 12 B1142392 B1142392 SNOV3MCM
992      11.8      40.7      64 13 BQ613346 BQ613346 rd30e01.y
993      11.8      40.7      64 14 CF293054 CF293054 3ODGS--02
994      11.8      40.7      64 28 AZ475718 AZ475718 1M0294D05
995      11.8      40.7      64 28 BZ290145 BZ290145 SALK 0235
996      11.8      40.7      64 29 CG552551 CG552551 OST162425
997      11.8      40.7      64 29 CG602220 CG602220 OST275422
998      11.8      40.7      64 29 CG650851 CG650851 OST409780
999      11.8      40.7      64 29 AG265379 AG265379 Lotus cor
1000     11.8      40.7      65 9   AI210398 AI210398 i0g06a1.r

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ALIGNMENTS

```

RESULT 1
AI561770      57 bp      mRNA      linear      EST 25-MAR-1999
LOCUS      v65b08.x1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION      IMAGE1227255 3', mRNA sequence.
ACCESSION      AI561770
VERSION      AI561770.1 GI:4513115
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
      1 (bases 1 to 57)
      Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
      Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
      Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
      Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
      Waterston,R. and Wilson,R.
      The WashU-NCI Mouse EST Project 1999
      Unpublished (1999)
      Contact: Marra M/WashU-NCI Mouse EST Project 1999

```

```

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousees@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:52847
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 51.
Location/Qualifiers
1..57
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1227255"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/notes="Organ: skin; Vector: pluscript SK-; Site: 1:
Ecoli; Site: 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
ORIGIN
Query Match      55.9%; Score 16.2; DB 9; Length 57;
Best Local Similarity 37.9%; Pred. No. 7.6e+04;
Matches 11; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
QY      1 UAUAUUCUUUUUUAAGCCUAGGCGGU 29
      :|||:||||:||||:||||:||||:
DB      25 TTGGAATCCCTTCTATCATCCATGGGGGT 53
      :|||:||||:||||:||||:||||:
RESULT 2
CB262321      77 bp      mRNA      linear      EST 06-NOV-2003
LOCUS      66-E8967-008-015-C18-PB12 MP1Z-ADIS-008 Arabidopsis thaliana cDNA
DEFINITION      clone MP1Zp767C1815Q 5-PRIME, mRNA sequence.
ACCESSION      CB262321
VERSION      CB262321.1 GI:32887094
KEYWORDS      EST.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
      rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
      1 (bases 1 to 77)
      Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
      Mitchell-Olds,T. and Weishaar,B.
      Large-scale identification and analysis of genome-wide
      single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
      Genome Res. 13 (6), 1250-1257 (2003)
      22893290
      12799357
      Contact: Weishaar B
      ADIS DNA core facility at MP1Z
      Max-Planck-Institute for Plant Breeding Research
      Carl-von-Linne Weg 10, 50829 Koeln, Germany
      Fax: 00492215062851
      Email: weishaar@mpiz-koeln.mpg.de
      Insert Length: 77 Std Error: 0.00
      Plate: 15 row: C column: 18
      Seq primer: PB12; GGTGGCGCCGCTCTAG.
      Location/Qualifiers
      1..77
      /organism="Arabidopsis thaliana"

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/mol_type="mRNA"
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/db_xref="taxon:3702"
/clone="MPIZp767C1815Q"
/tissue_type="seedling"
/dev_stage="few days old seedlings"
/lab_host="E. coli XLI-Blue MRF"
/clone_lib="MPIZ-ADIS-008"
/notes="Vector: pBluescript SK (-); Site 1: EcoRI; Site 2:
xhoI; cDNA library from Arabidopsis thaliana, accession
C24; seedling: Lambda ZAPII phage library was made at the
Max-Planck-Institute of Molecular Plant Physiology, Goltm,
Germany and mass-excised at the Max-Planck-Institute for
Plant Breeding Research, Cologne, Germany; cloning sites
EcoRI-XhoI; Note: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity.
'Etablissement of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection' PI: Bernd Weisshaar Sequence submission Managed
by RZPD/GABI-Primary database: http://gabi.rzpd.de This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."

```

ORIGIN

```

Query Match      55.9%; Score 16.2; DB 14; Length 77;
Best Local Similarity 37.9%; Pred. No. 7.3e+04;
Matches 11; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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Qy 1 UAUGAUUUUUUUUAAGCCUAGGGGCU 29
   : : : : : : : : : : : : : : : :
Db 22 TTTTITTTTTTTTGAACCAAGGGGTT 50

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RESULT 3

```

BH252676      77 bp DNA linear GSS 28-NOV-2001
LOCUS        SAUK_013733 Arabidopsis thaliana TDNA insertion lines Arabidopsis
DEFINITION   thaliana genomic clone SAUK_013733, genomic survey sequence.
ACCESSION    BH252676
VERSION      BH252676.1 GI:17139654
KEYWORDS     GSS.
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana

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```

REFERENCE     1 (bases 1 to 77)
AUTHORS       Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
              Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
              Shinn,P., Zimmerman,J. and Ecker,J.R.
              A Sequence-Indexed Library of Insertion Mutations in the
              Arabidopsis Genome
              Unpublished (2001)
              Contact: Joseph R. Ecker
              Salk Institute Genomic Analysis Laboratory (SIGnAL)
              The Salk Institute for Biological Studies
              10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
              Tel: 858 453 4100 x1752
              Fax: 858 558 6379
              Email: ecker@salk.edu

```

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

FEATURES

```

1..77
source
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SAUK_013733"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines"

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each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

```

Query Match      55.2%; Score 16; DB 28; Length 77;
Best Local Similarity 43.8%; Pred. No. 8.6e+04;
Matches 7; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AUGAUUUUUUUUUUA 17
   : : : : : : : : : : : : : : : :
Db 10 ATGATTCTTTTGTAA 25

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RESULT 4

```

CG590967      61 bp DNA linear GSS 02-OCT-2003
LOCUS        OST245023 Mus musculus 129Sv/Ev Mus musculus genomic clone
DEFINITION   OST245023, genomic survey sequence.
ACCESSION    CG590967
VERSION      CG590967.1 GI:37398378
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

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REFERENCE     1 (bases 1 to 61)
AUTHORS       Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
              Figgott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
              Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
              Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
              Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
              Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
              Zhu,Q., Person,C. and Sands,A.T.

```

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

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Location/Qualifiers
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ORIGIN

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Query Match      53.1%; Score 15.4; DB 29; Length 61;
Best Local Similarity 50.0%; Pred. No. 1.5e+05;
Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

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Qy 3 UGAUUCUUUUUUAAGCCUAGGGGC 28
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Db 58 TGAGCCTTTTTCAGCCCTAGTGCC 33

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RESULT 5

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TA123H02P/c
LOCUS        TA123H02P 66 bp DNA linear GSS 13-DEC-2000
DEFINITION   T. brucei sheared genomic DNA clone 123h02, forward sequence,
              genomic survey sequence.
ACCESSION    AL463084

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VERSION      AL463084.1  GI:11833690
KEYWORDS     GSS
SOURCE       Trypanosoma brucei
ORGANISM     Trypanosoma brucei
              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
              Trypanosoma.
REFERENCE    1 (bases 1 to 66)
AUTHORS      Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
              Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
              Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE        Direct Submission
JOURNAL      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
              project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
              Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
              nh1@sanger.ac.uk
COMMENT      Constructed at the Institute for Genomic Research (TIGR),
              Rockville, MD. Genomic DNA isolated from a cloned population of
              Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
              to give a tight size distribution (
              4 kb). The v + i method used for the library construction is
              described in detail in Smith, H. and Venter, J.C. (Making small
              insert libraries for whole genome shotgun sequencing projects. In
              Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999).
              Email: nelsayed@tigr.org
              Details of T. brucei sequencing at the Sanger Centre are available
              at http://www.sanger.ac.uk/Projects/T_brucei/.
              Location/Qualifiers
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              /clone="123h02"
ORIGIN
Query Match      53.1%; Score 15.4; DB 29; Length 66;
Best Local Similarity 36.0%; Pred. No. 1.5e+05;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUUGUAGCCCUAGG 25
   |||:::|||||
Db 30 TATGATTTTTCAGACCCCTAAG 6

RESULT 6
BM568281
LOCUS      sa102d02.y1 Gm-cl057 Glycine max cDNA clone SOYBEAN CLONE ID:
DEFINITION Gm-cl057-4011 5', mRNA sequence.
ACCESSION  BM568281
VERSION     BM568281.1  GI:18849172
KEYWORDS    Glycine max (soybean)
SOURCE      Glycine max
ORGANISM    Glycine max (soybean)

REFERENCE    1 (bases 1 to 73)
AUTHORS      Shoenaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvett, V.,
              Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
              Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
              Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
              Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
              McCann, R., Waterston, R. and Wilson, R.
              Public Soybean EST Project
              Unpublished (1999)
              Contact: Shoemaker R/Public Soybean EST Project
              Public Soybean EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800

QY 1 UAUGAUUUUUUUUGUAGCCCUAGG 25
   |||:::|||||
Db 30 TATGATTTTTCAGACCCCTAAG 6

RESULT 7
CB210991/c
LOCUS      OML01271 Oryza minuta HybridZAP-2.1 XR library Oryza minuta cDNA 5',
DEFINITION mRNA sequence.
ACCESSION  CB210991
VERSION     CB210991.1  GI:28257082
KEYWORDS    EST.
SOURCE      Oryza minuta
ORGANISM    Oryza minuta
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
              Glycine.
REFERENCE    1 (bases 1 to 41)
AUTHORS      Shin, J.S.
TITLE        Oryza minuta HybridZAP-2.1 XR library
JOURNAL      Unpublished (2003)
COMMENT      Contact: Jeong Sheop Shin
              Plant Molecular Genetics
              Graduate School of Biotechnology, University of Korea
              136-701 Anan-dong 5/1 Seoul, Korea
              Tel: 00 82 2 3290 3430
              Fax: 00 82 2 927 9028
              Email: jsshin@kucn.korea.ac.kr.
              Location/Qualifiers
FEATURES     source
              1..41
              /organism="Oryza minuta"
              /mol_type="mRNA"
              /db_xref="taxon:63629"
              /dev_stage="4-weeks after germination"
              /clone_lib="Oryza minuta HybridZAP-2.1 XR library"

```

```

Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4563 or contact: ccu@resgen.com web site:
www.resgen.com
Putative full length read
vector to vector length is 74
Seq primer: -40RP from Gibco.
Location/Qualifiers
FEATURES     source
              1..73
              /organism="Glycine max"
              /mol_type="mRNA"
              /db_xref="taxon:3847"
              /clone="SOYBEAN CLONE ID: Gm-cl057-4011"
              /tissue_type="Degenerating cotyledons, 2 week old
              seedling"
              /lab_host="DH10B"
              /clone_lib="Gm-cl057"
              /note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
              XhoI; The cDNA library was constructed from mRNA isolated
              from degenerating cotyledons of 2 week old seedlings from
              PI468916. Complementary DNA was synthesized from mRNA
              using a primer consisting of a poly(dT) sequence with a
              XhoI restriction site. EcoRI adapters were ligated to the
              blunt-ended cDNA fragments followed by XhoI digestion.
              The cDNA fragments were directionally cloned into the
              EcoRI-XhoI restriction site of the pBluescript vector. The
              ligated cDNA fragments were transformed into DH10B host
              cells (GibcoBRL). This library was constructed in the
              laboratory of Dr. Randy Shoemaker."
ORIGIN
Query Match      53.1%; Score 15.4; DB 12; Length 73;
Best Local Similarity 44.0%; Pred. No. 1.5e+05;
Matches 11; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUUGUAGCCCUAGG 25
   |||:::|||||
Db 19 TAAGCTTCCTTATTATAACCCAGG 43

RESULT 7
CB210991/c
LOCUS      OML01271 Oryza minuta HybridZAP-2.1 XR library Oryza minuta cDNA 5',
DEFINITION mRNA sequence.
ACCESSION  CB210991
VERSION     CB210991.1  GI:28257082
KEYWORDS    EST.
SOURCE      Oryza minuta
ORGANISM    Oryza minuta
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 41)
AUTHORS      Shin, J.S.
TITLE        Oryza minuta HybridZAP-2.1 XR library
JOURNAL      Unpublished (2003)
COMMENT      Contact: Jeong Sheop Shin
              Plant Molecular Genetics
              Graduate School of Biotechnology, University of Korea
              136-701 Anan-dong 5/1 Seoul, Korea
              Tel: 00 82 2 3290 3430
              Fax: 00 82 2 927 9028
              Email: jsshin@kucn.korea.ac.kr.
              Location/Qualifiers
FEATURES     source
              1..41
              /organism="Oryza minuta"
              /mol_type="mRNA"
              /db_xref="taxon:63629"
              /dev_stage="4-weeks after germination"
              /clone_lib="Oryza minuta HybridZAP-2.1 XR library"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0277 row: P column: 20
Seq Primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
FEATURES
source
1..25
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0277P20"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWP42 (G14732114|GB|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match 51.0%; Score 14.8; DB 28; Length 25;
Best Local Similarity 72.2%; Pred. No. 2.9e+05;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 11 UUUGUAGCCCUAGGGGC 28
Db 21 TTTCAGCCCAAGGGGC 4
:::|||||
RESULT 11
BE871815 60 bp mRNA linear EST 20-OCT-2000
LOCUS 601447803F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851880 5',
mRNA sequence.
BE871815
ACCESSION BE871815
VERSION BE871815.1 GI:10320591
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 60)
REFERENCE
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9573 row: e column: 01
High quality sequence stop: 60.
FEATURES
source
1..60
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="INAGE:3851880"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_65"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 51.0%; Score 14.8; DB 10; Length 60;
Best Local Similarity 38.9%; Pred. No. 2.5e+05;
Matches 7; Conservative 9; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AUGAUUUUUUUUAAGC 19
Db 10 AGGATTATTTCTAAGC 27
:::|||||
RESULT 12
BE003595/c 64 bp DNA linear GSS 04-DEC-2002
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-373C10-017165,
genomic survey sequence.
BE003595
ACCESSION BE003595
VERSION BE003595.1 GI:26188555
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
and Weisshaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 64)
Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
Direct Submission
Submitted (04-DEC-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene Atlg33610. The

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sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

Location/Qualifiers

1..64

/organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-373C10-017165"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

ORIGIN

Query Match 51.0%; Score 14.8; DB 29; Length 64;
 Best Local Similarity 34.6%; Pred. No. 2.5e+05;
 Matches 9; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

2 AUGAUUUUUUUUAAGCCCUAGGG 27

60 ATCTTTTATATGCTTGGG 35

RESULT 13

CD925111/c

LOCUS 66 bp mRNA linear EST 15-JUL-2003
 DEFINITION G750.115007F010706 G750 Triticum aestivum cDNA clone G750115007,
 mRNA sequence.

ACCESSION CD925111

VERSION CD925111.1

KEYWORDS GI:32772875

SOURCE EST.

ORGANISM Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Triticum.

1 (bases 1 to 66)

Genoplante.

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).

FEATURES

source

1..66

/organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="recital"
 /db_xref="taxon:4565"
 /clone="G750115007"
 /tissue_type="grain (750 degrees per day after
 pollination)"
 /clone_lib="G750"

ORIGIN

Query Match 51.0%; Score 14.8; DB 14; Length 66;
 Best Local Similarity 38.5%; Pred. No. 2.5e+05;
 Matches 10; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY

Db

RESULT 14

BMI28463

LOCUS

DEFINITION

69 bp mRNA linear EST 12-MAR-2002

if15c05.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens

cDNA clone IMAGE:5676297 3', mRNA sequence.

ACCESSION BMI28463

VERSION BMI28463.1

KEYWORDS GI:17123015

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 69)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Bliscain,A.,

Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,

Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R.,

Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Juliana Brown

(brown@fas.harvard.edu) This sequence now available from the IMAGE

consortium, for clone orders contact: info@image.llnl.gov.

Location/Qualifiers

1..69

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5676297"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;

Site 2: Sal 1; Starting library constructed using

SuperScript Plasmid library kit (Life Technologies). cDNA

made by oligo-dT priming. Size-selected by column

fractionation; average insert size 1.08 kb. Library was

amplified once on solid support and plasmid DNA from

library was prepared. The library DNA was normalized by

method #4 from Bonaldo, Lennon, and Soares 1996 Genome

Research 6:791-806; 0.5 microgram single-stranded library

plasmid DNA was mixed with 5 micrograms PCR product

representing library inserts and hybridized to an Ecot of

20. Single-stranded (unhybridized) plasmids were isolated

by hydroxyapatite chromatography and used to make this

library."

ORIGIN

Query Match

Best Local Similarity 51.0%; Score 14.8; DB 12; Length 69;

Matches 8; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY

Db

1

UNGAUUCUUUUUAAGCCCUAGGG 26

1

UNGAUUCUUUUUAAGCCCUAGGG 26

```

Db      8 TTTTTCCTTTTCCTGGCCCTAGGG 33

RESULT 15
BZ763921/c
LOCUS   72 bp DNA linear GSS 13-MAR-2003
DEFINITION
SALK_122786.15.90.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_122786.15.90.n, genomic
survey sequence.
ACCESSION
BZ763921
VERSION 1.1 GI:28936474
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1. (bases 1 to 72)
REFERENCE
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
CONTACT: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
1..72
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_122786.15.90.n"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 51.0%; Score 14.8; DB 28; Length 72;
Best Local Similarity 34.6%; Pred. No. 2.4e+05;
Matches 9; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 URAGUUCUUUUUUAAGCCCUAGG 26
:||||:||||:||||:||||:
55 TCTGATGATTTTATATGTTCTAGG 30

RESULT 16
TA185E01P/c
LOCUS   72 bp DNA linear GSS 13-DEC-2000
DEFINITION
T. brucei sheared genomic DNA clone 185e01, forward sequence,
genomic survey sequence.
ACCESSION
AL474065
VERSION 1.1 GI:11840836
KEYWORDS
SOURCE
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1. (bases 1 to 72)
REFERENCE
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
FEATURES
Location/Qualifiers
1..72
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="185e01"
ORIGIN
Query Match 51.0%; Score 14.8; DB 29; Length 72;
Best Local Similarity 61.1%; Pred. No. 2.4e+05;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 12 UUGUAGGCCCUAGGGGCU 29
:||||:||||:||||:
66 TTCTAAGCCATAGGGGCT 49

RESULT 17
AZ775013/c
LOCUS   73 bp DNA linear GSS 16-FEB-2001
DEFINITION
2M0004K20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0004K20 R, genomic survey sequence.
ACCESSION
AZ775013
VERSION 1.1 GI:12901065
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1. (bases 1 to 73)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0004 row: K column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 73.
Location/Qualifiers
1..73
/organism="Mus musculus"
FEATURES
source

```

/mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0004K20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /clone_lib="Mouse 10kb Plasmid UUGCLM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.0%; Score 14.8; DB 28; Length 73;
 Best Local Similarity 61.1%; Pred. No. 2.4e+05;
 Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 11 UUUUAGGCCUAGGGCC 28
 : : : : :
 Db 18 TTGTATACCTAGGGCC 1

RESULT 18
 AI819570/c
 LOCUS
 DEFINITION
 w191q08.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2410238 3', similar to gb:X57958 60S RIBOSOMAL PROTEIN L7 (HUMAN);, mRNA

ACCESSION AI819570
 VERSION AI819570.1 GI:5438649
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 74)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Life Technologies catalog #: 11547-015

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 195 Std Error: 0.00

Seq primer: -40up from Gbco.

Location/Qualifiers

1..74

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2410238"

/issue_type="lymphoma, follicular mixed small and large cell"

/lab_host="DH10B"

/clone_lib="NCI CGAP Lym12"
 /note="Organ: lymph node; Vector: pCMV-Sport6; Site: 1; Salt; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

ORIGIN

Query Match 51.0%; Score 14.8; DB 9; Length 74;
 Best Local Similarity 38.9%; Pred. No. 2.4e+05;
 Matches 7; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 2 AUGAUUCUUUUGUAGGC 19

|||: : : : :
 Db 54 ATGATTATTTTCTAGC 37

RESULT 19

AA975663/c

LOCUS

DEFINITION
 oq63f07.s1 NCI CGAP Kid6 Homo sapiens cDNA clone IMAGE:1591045 3', similar to gb:X57958 60S RIBOSOMAL PROTEIN L7 (HUMAN);, mRNA

sequence.

ACCESSION AA975663

VERSION AA975663.1 GI:3151455

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 76)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: L. Jeffrey Medeiros, M.D.; Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Stratagene, Inc.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 436 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES

source

1..76

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1591045"

/sex="mixed"

/tissue_type="kidney tumor"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="NCI CGAP Kid6"

/note="Organ: kidney; Vector: Bluescript SK-; Site: 1;

ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:

Oligo dt. Pooled kidney tumors. 5' adaptor sequence: 5'

GAATTCGGCAGCAG 3' 3' adaptor sequence: 5'

CTCAGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."

ORIGIN

Query Match 51.0%; Score 14.8; DB 9; Length 76;
 Best Local Similarity 38.9%; Pred. No. 2.4e+05;
 Matches 7; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 2 AUGAUUCUUUUGUAGGC 19

|||: : : : :
 Db 49 ATGATTATTTTCTAGC 32

RESULT 20


```

OST152329, genomic survey sequence.
CG549254
VERSION CG549254.1 GI:37335841
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 77)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
    source
        Location/Qualifiers
            1..77
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="129SV/Ev"
                /db_xref="taxon:10090"
                /clone="OST152329"
                /cell_type="embryonic stem cell"
                /clone_lib="Mus musculus 129SV/Ev"
ORIGIN
Query Match 51.0%; Score 14.8; DB 29; Length 77;
Best Local Similarity 44.4%; Pred. No. 2.4e+05;
Matches 8; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
QY 2 AUGAUUUUUUGUAGC 19
| : : : : : : : : : :
Db 6 AGGATCTTTTCTAAGC 23
| : : : : : : : : : :
RESULT 23
BX287070
LOCUS BX287070 49 bp DNA linear GSS 07-MAR-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-396F11-018295,
Genomic survey sequence.
ACCESSION BX287070
VERSION BX287070.1 GI:28886066
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Siedler,H.
and Weishaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
JOURNAL
REFERENCE
2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weishaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
JOURNAL
REFERENCE
3 (bases 1 to 49)
OST152329, genomic survey sequence.
CG549254
VERSION CG549254.1 GI:37335841
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 77)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
    source
        Location/Qualifiers
            1..77
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="129SV/Ev"
                /db_xref="taxon:10090"
                /clone="OST152329"
                /cell_type="embryonic stem cell"
                /clone_lib="Mus musculus 129SV/Ev"
ORIGIN
Query Match 51.0%; Score 14.8; DB 29; Length 77;
Best Local Similarity 44.4%; Pred. No. 2.4e+05;
Matches 8; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
QY 2 AUGAUUUUUUGUAGC 19
| : : : : : : : : : :
Db 6 AGGATCTTTTCTAAGC 23
| : : : : : : : : : :
RESULT 23
BX287070
LOCUS BX287070 49 bp DNA linear GSS 07-MAR-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-396F11-018295,
Genomic survey sequence.
ACCESSION BX287070
VERSION BX287070.1 GI:28886066
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Siedler,H.
and Weishaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
JOURNAL
REFERENCE
2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weishaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
JOURNAL
REFERENCE
3 (bases 1 to 49)
Strizhov,N., Li,Y., Rosso,M. and Weishaar,B.
Direct Submission
Submitted (07-MAR-2003) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone MZ24. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
    source
        Location/Qualifiers
            1..49
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /strain="Columbia 0"
                /db_xref="taxon:3702"
                /clone="GK-396F11-018295"
                /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                /note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"
ORIGIN
Query Match 50.3%; Score 14.6; DB 29; Length 49;
Best Local Similarity 41.4%; Pred. No. 3.1e+05;
Matches 12; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
QY 1 UAUUAUUUUUUUUAAGCCUAGGGGCU 29
| : : : : : : : : : :
Db 8 TAAGCTTAATGTGTGAAGGCTATGGAT 36
| : : : : : : : : : :
RESULT 24
BG236504
LOCUS BG236504 52 bp mRNA linear EST 12-FEB-2001
DEFINITION nai44c06.x1 NCI_CGAP_HN20 Homo sapiens cDNA clone IMAGE:4262795 3',
mRNA sequence.
ACCESSION BG236504
VERSION BG236504.1 GI:12750351
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 52)
NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco.
Location/Qualifiers
    source
        Location/Qualifiers
            1..52
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4262795"
                /lab_host="DH10B"
                /clone_lib="NCI_CGAP_HN20"

```


/lab host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /clone lib="Mouse 10kb plasmid UGCM1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 50.3%; Score 14.6; DB 28; Length 66;
 Best Local Similarity 52.4%; Pred. No. 3e+05;
 Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 8 CUUUUUAAGCCCUAGGGCC 28

Db 18 CTTCTGTACACCCPAGGGCC 38

RESULT 30

B1865610/c

LOCUS

DEFINITION

ft22h02.y1 Zebrafish neuronal Danio rerio cDNA clone IMAGE:5082459

5', mRNA sequence.

ACCESSION

B1865610

VERSION

B1865610.1

KEYWORDS

EST

SOURCE

Danio rerio (zebrafish)

ORGANISM

Danio rerio

REFERENCE

AUTHORS

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,

Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, J.,

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R., and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

Other ESTs: ft22h02.x1

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@wustl.edu

CDNA Library constructed by S. Lin DNA Sequencing by: Washington

University Genome Sequencing Center Clone distribution: the

I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov

Seq primer: T3 ET from Amersham.

Location/Qualifiers

1..73

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:5082459"

/sex="mixed"

/dev_stage="adult"

FEATURES

source

/lab host="DH10B (phage-resistant)"
 /clone lib="Zebrafish neuronal"
 /note="Organ: brain; Vector: pBluescript (modified);
 Site 1: DraIII(V); Site 2: DraIII(X); Library is cloned
 directionally between the DraIII(X) and DraIII(V) sites
 and has been amplified. Library constructed by S. Lin."

ORIGIN

Query Match 50.3%; Score 14.6; DB 12; Length 73;
 Best Local Similarity 27.6%; Pred. No. 2.9e+05;
 Matches 8; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 UUAUAUUUUUUUAAGCCCUAGGGCCU 29

Db 59 TTTTTTTTTTTTTTGAGCTCTTCGGGCT 31

RESULT 31

BX001193

LOCUS

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence GK-104G08-018339,

genomic survey sequence.

ACCESSION

BX001193

VERSION

BX001193.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1

Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.

and Weisshaar, B.

A pipeline for automated high-throughput generation of ESTs

(flanking sequence tags) from Arabidopsis thaliana T-DNA

transformed lines

Unpublished

2

Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.

A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)

for flanking sequence tag based reverse genetics

Unpublished

3 (bases 1 to 73)

Direct Submission

Submitted (04-DEC-2002) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion within the locus defined by clone T22B15.

The sequences are generated at the MPI for Plant Breeding Research

in the context of the GABI-Kat project. GABI-Kat is part of the

German Plant Genomics program designated 'GABI'. Information on

line availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1..73

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-104G08-018339"

/clone lib="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on DNA from Arabidopsis thaliana

plants (T1) which were transformed with the T-DNA from

vector PAC161. The lines contain one or more T-DNA from

insertions. The DNA fragment(s) resulting from the PCR

were directly sequenced to determine the genomic sequence

flanking the insertion. Sequences displaying significant

similarity to the A. thaliana nuclear genome sequence were

processed for submission. T-DNA derived sequences were

removed"

ORIGIN


```

Query Match      50.3%; Score 14.6; DB 29; Length 73;
Best Local Similarity 37.9%; Pred. No. 2.9e+05;
Matches 11; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 UGAUUCUUUUUGUAGCCUAGGGCCU 29
   : : : : : : : : : : : : : : : :
Db 43 TGTGATATTATTAGAAACCTATGGGAT 71

RESULT 32
LOCUS D11626
DEFINITION HUMOC13G12 Liver HepG2 cell line. Homo sapiens cDNA clone c13g12,
mRNA sequence.
ACCESSION D11626
VERSION D11626.1 GI:2148761
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 79)
TITLE Okubo,K., Hori,N., Matoba,R., Niiyama,T., Fukushima,A., Kojima,Y.
and Matsubara,K.
JOURNAL Large scale cDNA sequencing for analysis of quantitative and
MEDLINE qualitative aspects of gene expression
PUBMED Nat. Genet. 2, 173-179 (1992)
94258199
1345164
COMMENT Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki
Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
Institute for Molecular and Cellular Biology
Osaka University
1-3 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES
source
1..79
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:D058126E"
/db_xref="taxon:9606"
/clone="c13g12"
/lab_host="E. coli"
/clone_lib="Liver HepG2 cell line."
/notes="3'-directed regional cDNA library. Cleaved by MhoI
and transformed into E.coli."

ORIGIN
Query Match      50.3%; Score 14.6; DB 14; Length 79;
Best Local Similarity 33.3%; Pred. No. 2.9e+05;
Matches 7; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 3 UGAUUCUUUUUGUAGCCCUA 23
   : : : : : : : : : : : :
Db 12 TGTATTGTTTGTGAATCCATA 32

RESULT 33
LOCUS BH910631/c
DEFINITION SALK_060727.15.15.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_060727.15.15.x, genomic
survey sequence.
ACCESSION BH910631
VERSION BH910631.1 GI:22723564
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 31)
REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
AUTHORS Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..31
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_060727.15.15.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      49.7%; Score 14.4; DB 28; Length 31;
Best Local Similarity 41.7%; Pred. No. 4e+05;
Matches 10; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 3 UGAUUCUUUUUGUAGCCCUAGG 26
   : : : : : : : : : : : :
Db 31 TTAATGTCCTGTGAAGACCTAGTG 8

RESULT 34
LOCUS AZ597048/c
DEFINITION 1M0410K10R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0410K10 R, genomic survey sequence.
ACCESSION AZ597048
VERSION AZ597048.1 GI:11719238
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 43)
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
AUTHORS Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0410 row: K column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: Plasmid ends
High quality sequence stop: 43.
Location/Qualifiers

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/note="Organ: brain; Vector: pBluescript (modified);
Site 1: DraIII(X); Site 2: DraIII(X); Library is cloned
directionally between the DraIII(X) and DraIII(Y) sites
and has been amplified. Library constructed by S. Lin."

ORIGIN
Query Match          49.7%; Score 14.4; DB 12; Length 54;
Best Local Similarity 33.3%; Pred. No. 3.6e+05;
Matches 8; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 6 UUCUUUUUUAAGCCCUAGGGGCU 29
Db 5 TTTTITTTTGGAGCTCTCGGGCT 28

RESULT 37
AL595218
LOCUS AL595218 XGC-gastrula Silurana tropicalis cDNA clone TGas002h22 5',
DEFINITION mRNA sequence.
ACCESSION AL595218
VERSION AL595218.1 GI:15007293
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 60)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
Contact: Huckle E
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
TROPICALIS SEQUENCE ID: TGas002h22.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from Sug of poly A+ RNA from stages 10-13
gastrulae. EcoRI-NotI cut cDNA was then ligated into pCSI07 with
EcoRI at the 5' end and NotI at the 3' end.
Vector: pCSI07; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
Host: Escherichia coli XL1-blue.

FEATURES
source
1..60
Location/Qualifiers
/organism="Silurana tropicalis"
/mol_type="mRNA"
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/clone="TGas002h22"
/dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-gastrula"
/note="Vector: pCSI07; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCSI07 with EcoRI at the 5' end and NotI at the 3'
end."

ORIGIN
Query Match          49.7%; Score 14.4; DB 9; Length 60;
Best Local Similarity 37.5%; Pred. No. 3.6e+05;
Matches 9; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 2 AUGAUUUUUUUAAGCCCUAGG 25
Db 8 ATGATTTTATTGTTCTTCTAG 31

RESULT 38
BG362434/c

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LOCUS BG362434 63 bp mRNA linear EST 08-MAR-2001
DEFINITION GB72b09.Y1 Moss EST library PPG Physcomitrella patens cDNA clone
PEP SOURCE_ID: 5', mRNA sequence.
ACCESSION BG362434
VERSION BG362434.1 GI:13251531
KEYWORDS EST.
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 63)
Quatrano,R., Bashardes,S., Cove,D., Cumming,A., Knight,C.,
Clifton,S., Marta,M., Hillier,L., Pape,D., Martin,J., Wylie,T.,
Underwood,K., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Steptoe,M., Gibbons,M., Harvey,N., Ritter,E.,
Jackson,Y., McCann,K., Waterston,K. and Wilson,R.
Leeds/Wash U Moss EST Project
Unpublished (1999)
Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Libraries were constructed by Dr. Stavros Bashardes as part of the
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Seq primer: -40RP from Gibco.
Location/Qualifiers
1..63
/organism="Physcomitrella patens"
/mol_type="mRNA"
/db_xref="taxon:3218"
/clone="PEP_SOURCE_ID:"
/tissue_type="gametophore: 30 day old tissue,
ammonium-grown"
/lab_host="DH10B"
/clone_lib="Moss EST library PPG"
/note="Vector: pAMP1; Construction of the cDNA library was
performed by Dr. W. Gregg Clark using a modification of
the cDNA synthesis protocol developed in the laboratory of
Dr. Michael Lovett by Dr. Yulia Korshunova (personal
communication). First polyA+ RNA was isolated from total
gametophore RNA using oligo dT magnetic beads. Following
this, first strand cDNA synthesis was performed on the
bead-bound polyA+ RNA, during which an oligonucleotide
anchor sequence was incorporated onto the 5'-ends of the
cDNA. PCR amplification was then used to synthesize the
second strand, to amplify the double stranded DNA, and to
incorporate dUTP containing sequences into the ends of the
double stranded cDNA. This DNA was size selected and
cloned into pAMP1 using the CloneAMP pAMP1 System (Life
Technologies GibcoBRL) for cloning amplification products
by a non-restriction site dependant process. The cloning
was directional based on sequence asymmetry, introduced at
the ends during PCR amplification. The 3' cDNA ends are
proximal to the NotI site of the multiple cloning site in
pAMP1. This annealing mixture was transformed into
chemically competent DH10B cells and selected for
ampicillin resistant growth. The resulting clones (about
330,000) were pooled to make the library."

ORIGIN
Query Match          49.7%; Score 14.4; DB 12; Length 63;
Best Local Similarity 33.3%; Pred. No. 3.5e+05;
Matches 8; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUAAGCCCUAG 24
Db 42 TTTTITTTTITTTTGAACCCCAAG 19

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RESULT 39
CG664319/c
LOCUS
DEFINITION
OS7451176 Mus musculus 129Sv/Ev Mus musculus genomic clone
OS7451176, genomic survey sequence.
ACCESSION
CG664319
VERSION
CG664319.1 GI:37489168
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 65)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
source
1..65
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/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST451176"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 49.7%; Score 14.4; DB 29; Length 65;
Best Local Similarity 33.3%; Pred. No. 3.5e+05;
Matches 8; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 6 UUCUUUUGUAGGCCUAGGGGCU 29
:::|||||:|:|:|:
Db 63 TTTTGTGATAGATCTCTGGGTT 40

RESULT 40
AI584052/c
LOCUS
DEFINITION
AI584052 67 bp mRNA linear EST 14-DEC-1999
ts13b02.x1 NCI CGAP Panel Homo sapiens cDNA clone IMAGE:2228427 3'
similar to TR.000599 O00599 CON1; contains element MER22
repetitive element 1, mRNA sequence.

ACCESSION
AI584052
VERSION
AI584052.1 GI:4569949
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 67)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1154 Std Error: 0.00
Seq Primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.

FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2228427"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Panel"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

ORIGIN

Query Match 49.7%; Score 14.4; DB 9; Length 67;
Best Local Similarity 37.5%; Pred. No. 3.5e+05;
Matches 9; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUCUUUUUUAAGGCCUAGGGG 27
|:::|||||:|:|:|:
Db 38 GGTGTTTTTTTTTTCCTAGGGG 15

Search completed: April 18, 2004, 09:59:04
Job time: 1568.67 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 07:34:53 ; Search time 36.6667 Seconds
(without alignments)
438.916 Million cell updates/sec

Title: US-09-310-844C-25

Perfect score: 29

Sequence: 1 aaagaucuuuuuuaagcccaagggcu 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 915622

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
C 1	15.2	52.4	33	Sequence 5, Appl
C 2	15.2	52.4	47	Sequence 1097, Ap
C 3	15.2	52.4	75	Sequence 6, Appl
C 4	14.8	51.0	29	Sequence 25, Appl
C 5	14.8	51.0	29	Sequence 25, Appl
C 6	14.8	51.0	29	Sequence 25, Appl
C 7	14.8	51.0	29	Sequence 25, Appl
C 8	14.8	51.0	29	Sequence 25, Appl
C 9	14.8	51.0	29	Sequence 25, Appl
C 10	14.8	51.0	29	Sequence 25, Appl
C 11	14.8	51.0	29	Sequence 25, Appl
C 12	14.8	51.0	29	Sequence 25, Appl
C 13	14.6	50.3	25	Sequence 18, Appl
C 14	14.6	50.3	25	Sequence 18, Appl
C 15	14.2	49.0	25	Sequence 18, Appl
C 16	14.2	49.0	25	Sequence 18, Appl
C 17	14.2	49.0	25	Sequence 18, Appl
C 18	14.2	49.0	25	Sequence 18, Appl
C 19	14.2	49.0	25	Sequence 18, Appl
C 20	14.2	49.0	25	Sequence 18, Appl
C 21	14.2	49.0	25	Sequence 18, Appl
C 22	14.2	49.0	25	Sequence 18, Appl
C 23	14.2	49.0	25	Sequence 18, Appl
C 24	14.2	49.0	25	Sequence 18, Appl
C 25	14.2	49.0	25	Sequence 18, Appl
C 26	14.2	49.0	25	Sequence 18, Appl
C 27	14.2	49.0	25	Sequence 18, Appl

C 28	13.8	47.6	25	3	US-08-943-731-336	Sequence 336, App
C 29	13.8	47.6	33	4	US-09-199-542B-76	Sequence 76, Appl
C 30	13.8	47.6	47	4	US-09-671-317-663	Sequence 663, App
C 31	13.8	47.6	50	4	US-09-428-082B-401	Sequence 401, App
C 32	13.8	47.6	57	4	US-09-428-082B-414	Sequence 414, App
C 33	13.8	47.6	60	4	US-09-428-082B-415	Sequence 415, App
C 34	13.8	47.6	61	4	US-09-428-082B-400	Sequence 400, App
C 35	13.6	46.9	41	4	US-09-565-156A-2	Sequence 2, Appl
C 36	13.6	46.9	47	4	US-09-422-978-1843	Sequence 1843, Ap
C 37	13.6	46.9	47	4	US-09-402-266B-10	Sequence 10, Appl
C 38	13.6	46.9	52	4	US-09-310-463-6	Sequence 6, Appl
C 39	13.6	46.9	52	4	US-08-842-248A-6	Sequence 6, Appl
C 40	13.6	46.9	79	1	US-08-472-255A-136	Sequence 136, App
C 41	13.6	46.9	79	1	US-08-479-724A-136	Sequence 136, App
C 42	13.6	46.9	79	3	US-08-472-256B-136	Sequence 136, App
C 43	13.6	46.9	79	3	US-08-952-793-136	Sequence 136, App
C 44	13.6	46.9	79	4	US-09-849-928-136	Sequence 136, App
C 45	13.6	46.9	79	5	PCT-US96-09455A-136	Sequence 136, App
C 46	13.4	46.2	32	3	US-08-718-738-16	Sequence 16, Appl
C 47	13.4	46.2	32	3	US-09-221-844-16	Sequence 16, Appl
C 48	13.4	46.2	32	5	PCT-US95-03323A-16	Sequence 16, Appl
C 49	13.4	46.2	40	4	US-09-428-082B-418	Sequence 418, App
C 50	13.4	46.2	46	1	US-08-171-389-42	Sequence 42, Appl
C 51	13.4	46.2	46	1	US-08-171-389-45	Sequence 45, Appl
C 52	13.4	46.2	46	1	US-08-123-936-42	Sequence 42, Appl
C 53	13.4	46.2	46	1	US-08-123-936-45	Sequence 45, Appl
C 54	13.4	46.2	46	2	US-08-475-228A-42	Sequence 42, Appl
C 55	13.4	46.2	46	2	US-08-475-228A-45	Sequence 45, Appl
C 56	13.4	46.2	46	3	US-08-482-080A-42	Sequence 42, Appl
C 57	13.4	46.2	46	3	US-08-482-080A-45	Sequence 45, Appl
C 58	13.4	46.2	46	4	US-09-354-947-42	Sequence 42, Appl
C 59	13.4	46.2	46	4	US-09-354-947-45	Sequence 45, Appl
C 60	13.4	46.2	46	5	PCT-US93-12388-42	Sequence 42, Appl
C 61	13.4	46.2	46	5	PCT-US93-12388-45	Sequence 45, Appl
C 62	13.4	46.2	50	1	US-08-245-754A-13	Sequence 13, Appl
C 63	13.4	46.2	50	1	US-08-171-389-46	Sequence 46, Appl
C 64	13.4	46.2	50	1	US-08-123-936-46	Sequence 46, Appl
C 65	13.4	46.2	50	2	US-08-475-228A-46	Sequence 46, Appl
C 66	13.4	46.2	50	2	US-08-597-731-13	Sequence 13, Appl
C 67	13.4	46.2	50	3	US-08-482-080A-46	Sequence 46, Appl
C 68	13.4	46.2	50	4	US-09-354-947-46	Sequence 46, Appl
C 69	13.4	46.2	50	5	PCT-US93-12388-46	Sequence 46, Appl
C 70	13.2	45.5	22	3	US-08-969-317-9	Sequence 9, Appl
C 71	13.2	45.5	25	4	US-08-827-998-1097	Sequence 1097, Ap
C 72	13.2	45.5	25	4	US-08-827-998-1105	Sequence 1105, Ap
C 73	13.2	45.5	27	1	US-08-485-602-23	Sequence 23, Appl
C 74	13.2	45.5	27	1	US-08-757-180-22	Sequence 22, Appl
C 75	13.2	45.5	27	1	US-08-745-638-23	Sequence 23, Appl
C 76	13.2	45.5	29	4	US-09-304-232-120	Sequence 120, App
C 77	13.2	45.5	29	4	US-09-304-232-344	Sequence 344, App
C 78	13.2	45.5	32	4	US-09-031-889A-12	Sequence 12, Appl
C 79	13.2	45.5	38	1	US-08-372-224A-1480	Sequence 1480, Ap
C 80	13.2	45.5	38	1	US-08-435-628-1480	Sequence 1480, Ap
C 81	13.2	45.5	38	2	US-09-292-620A-2069	Sequence 2069, Ap
C 82	13.2	45.5	38	3	US-09-071-845-2069	Sequence 2069, Ap
C 83	13.2	45.5	47	4	US-08-422-978-1851	Sequence 1851, Ap
C 84	13.2	45.5	64	1	US-08-271-364A-2	Sequence 2, Appl
C 85	13.2	45.5	66	4	US-08-956-171B-2731	Sequence 2731, Ap
C 86	13.2	45.5	69	4	US-09-732-210-25	Sequence 25, Appl
C 87	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 88	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 89	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 90	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 91	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 92	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 93	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 94	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 95	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 96	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 97	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 98	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 99	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App
C 100	13.2	45.5	69	4	US-08-758-306-320	Sequence 320, App

101	13	44.8	70	5	PCT-US96-09472-157	Sequence 157, App	174	12.6	43.4	45	1	US-08-171-389-342	Sequence 342, App
102	13	44.8	78	1	US-08-400-256-11	Sequence 11, Appl	175	12.6	43.4	45	1	US-08-123-936-130	Sequence 130, App
103	13	44.8	78	3	US-08-975-365-11	Sequence 11, Appl	176	12.6	43.4	45	1	US-08-123-936-342	Sequence 342, App
104	12.8	44.1	18	4	US-09-422-978-5466	Sequence 5466, Ap	177	12.6	43.4	45	2	US-08-475-228A-130	Sequence 130, App
105	12.8	44.1	20	2	US-09-289-368-95	Sequence 85, Appl	178	12.6	43.4	45	2	US-08-475-228A-342	Sequence 342, App
106	12.8	44.1	20	4	US-09-323-357-18	Sequence 18, Appl	179	12.6	43.4	45	3	US-08-482-080A-130	Sequence 130, App
107	12.8	44.1	24	4	US-09-013-160-75	Sequence 75, Appl	180	12.6	43.4	45	3	US-08-482-080A-342	Sequence 342, App
108	12.8	44.1	28	3	US-08-646-861-28	Sequence 28, Appl	181	12.6	43.4	45	4	US-08-290-995-4	Sequence 4, Appl
109	12.8	44.1	30	3	US-08-621-841-51	Sequence 51, Appl	182	12.6	43.4	45	4	US-09-354-947-130	Sequence 130, App
110	12.8	44.1	33	1	US-08-181-271A-96	Sequence 96, Appl	183	12.6	43.4	45	5	PCT-US93-12388-130	Sequence 342, App
111	12.8	44.1	33	1	US-08-449-315-96	Sequence 96, Appl	184	12.6	43.4	45	5	PCT-US93-12388-342	Sequence 342, App
112	12.8	44.1	33	1	US-08-444-803-96	Sequence 96, Appl	185	12.6	43.4	48	4	US-09-238-356-64	Sequence 64, Appl
113	12.8	44.1	33	1	US-08-094-534-20	Sequence 20, Appl	186	12.6	43.4	49	4	US-08-961-888-6	Sequence 7, Appl
114	12.8	44.1	33	1	US-08-449-043-96	Sequence 96, Appl	187	12.6	43.4	49	4	US-08-961-888-7	Sequence 7, Appl
115	12.8	44.1	33	1	US-08-456-265A-96	Sequence 96, Appl	188	12.6	43.4	49	4	US-08-961-888-7	Sequence 7, Appl
116	12.8	44.1	33	1	US-08-456-416-96	Sequence 96, Appl	189	12.6	43.4	50	1	US-08-171-389-343	Sequence 343, App
117	12.8	44.1	33	1	US-08-455-244-96	Sequence 96, Appl	190	12.6	43.4	50	2	US-08-123-936-343	Sequence 343, App
118	12.8	44.1	33	1	US-08-454-876-96	Sequence 96, Appl	191	12.6	43.4	50	2	US-08-475-228A-343	Sequence 343, App
119	12.8	44.1	33	2	US-08-457-364-96	Sequence 96, Appl	192	12.6	43.4	50	3	US-08-482-080A-343	Sequence 31, Appl
120	12.8	44.1	33	2	US-08-456-262-96	Sequence 96, Appl	193	12.6	43.4	50	4	US-09-390-867A-31	Sequence 31, Appl
121	12.8	44.1	33	2	US-08-456-240-96	Sequence 96, Appl	194	12.6	43.4	50	4	US-09-354-947-343	Sequence 343, App
122	12.8	44.1	33	2	US-08-455-716-96	Sequence 96, Appl	195	12.6	43.4	50	5	PCT-US93-12388-343	Sequence 343, App
123	12.8	44.1	33	2	US-08-971-217-96	Sequence 96, Appl	196	12.6	43.4	51	4	US-09-425-585-6	Sequence 6, Appl
124	12.8	44.1	33	2	US-08-581-543-20	Sequence 20, Appl	197	12.6	43.4	51	4	US-09-353-321-6	Sequence 6, Appl
125	12.8	44.1	33	3	US-09-350-600-96	Sequence 96, Appl	198	12.6	43.4	51	4	US-09-479-645A-188	Sequence 188, App
126	12.8	44.1	33	4	US-09-906-234-96	Sequence 96, Appl	199	12.6	43.4	52	2	US-08-464-073-22	Sequence 22, Appl
127	12.8	44.1	33	5	PCT-US94-08000-20	Sequence 20, Appl	200	12.6	43.4	62	2	US-08-428-253-22	Sequence 22, Appl
128	12.8	44.1	35	4	US-10-045-428A-16	Sequence 16, Appl	201	12.6	43.4	62	3	US-08-937-610-16	Sequence 16, Appl
129	12.8	44.1	36	1	US-08-319-492B-332	Sequence 332, App	202	12.6	43.4	62	3	US-08-416-516A-22	Sequence 22, Appl
130	12.8	44.1	40	2	US-08-423-684-58	Sequence 58, Appl	203	12.6	43.4	62	4	US-09-268-347-50	Sequence 50, Appl
131	12.8	44.1	40	2	US-08-675-503-58	Sequence 58, Appl	204	12.6	43.4	66	4	US-08-940-136-261	Sequence 261, App
132	12.8	44.1	40	4	US-09-245-803-58	Sequence 58, Appl	205	12.6	43.4	67	3	US-09-275-850-315	Sequence 315, App
133	12.8	44.1	43	3	US-09-306-998-16	Sequence 16, Appl	206	12.6	43.4	69	2	US-08-790-963-100	Sequence 100, App
134	12.8	44.1	47	4	US-09-422-978-2381	Sequence 2381, Ap	207	12.6	43.4	69	3	US-09-371-774-100	Sequence 100, App
135	12.8	44.1	48	2	US-08-477-553A-16	Sequence 16, Appl	208	12.6	43.4	71	3	US-09-275-850-94	Sequence 94, Appl
136	12.8	44.1	54	3	US-08-369-822C-30	Sequence 30, Appl	209	12.6	43.4	71	3	US-09-275-850-95	Sequence 95, Appl
137	12.8	44.1	54	3	US-08-582-776C-35	Sequence 45, Appl	210	12.6	43.4	72	2	US-08-464-073-20	Sequence 20, Appl
138	12.8	44.1	54	3	US-08-434-831B-27	Sequence 42, Appl	211	12.6	43.4	72	2	US-08-428-252-20	Sequence 20, Appl
139	12.8	44.1	54	4	US-09-315-926A-27	Sequence 27, Appl	212	12.6	43.4	72	2	US-08-416-516A-20	Sequence 20, Appl
140	12.8	44.1	61	1	US-08-702-795-3	Sequence 3, Appl	213	12.6	43.4	77	1	US-08-442-572-1	Sequence 1, Appl
141	12.8	44.1	69	3	US-08-483-511-77	Sequence 77, Appl	214	12.6	43.4	77	1	US-08-361-795-1	Sequence 1, Appl
142	12.8	44.1	71	1	US-08-131-365B-39	Sequence 39, Appl	215	12.6	43.4	77	5	PCT-US95-05600-84	Sequence 84, Appl
143	12.8	44.1	71	2	US-08-668-123-39	Sequence 3, Appl	216	12.6	43.4	78	3	US-08-945-734-73	Sequence 73, Appl
144	12.6	43.4	19	1	US-08-384-490-3	Sequence 3, Appl	217	12.6	43.4	78	3	US-09-258-797-77	Sequence 77, Appl
145	12.6	43.4	19	1	US-08-459-383-3	Sequence 3, Appl	218	12.6	43.4	78	3	US-09-445-283C-45	Sequence 45, Appl
146	12.6	43.4	23	4	US-09-470-661A-22	Sequence 22, Appl	219	12.4	42.8	22	4	US-09-033-055A-5	Sequence 5, Appl
147	12.6	43.4	25	3	US-08-692-787-76	Sequence 76, Appl	220	12.4	42.8	28	2	US-08-726-090-9	Sequence 9, Appl
148	12.6	43.4	25	3	US-09-304-232-781	Sequence 781, App	221	12.4	42.8	28	4	US-09-311-983-1	Sequence 1, Appl
149	12.6	43.4	29	4	US-08-894-808-8	Sequence 8, Appl	222	12.4	42.8	28	4	US-08-324-243-30	Sequence 30, Appl
150	12.6	43.4	35	1	US-08-041-538-3	Sequence 3, Appl	223	12.4	42.8	30	1	US-08-532-390-30	Sequence 30, Appl
151	12.6	43.4	35	1	US-08-463-642-3	Sequence 3, Appl	224	12.4	42.8	30	1	US-08-717-294-30	Sequence 30, Appl
152	12.6	43.4	35	1	US-08-455-602-3	Sequence 3, Appl	225	12.4	42.8	30	5	PCT-US95-11511-30	Sequence 7, Appl
153	12.6	43.4	35	2	US-08-465-157-3	Sequence 3, Appl	226	12.4	42.8	31	3	US-09-033-055A-7	Sequence 10, Appl
154	12.6	43.4	35	2	PCT-US91-09422-3	Sequence 3, Appl	227	12.4	42.8	33	4	US-09-622-540A-10	Sequence 10, Appl
155	12.6	43.4	35	5	5281520-10	Patent No. 5281520	228	12.4	42.8	33	4	US-09-622-540A-10	Sequence 2, Appl
156	12.6	43.4	36	2	US-08-882-083-7	Sequence 7, Appl	229	12.4	42.8	34	4	US-09-581-070-2	Sequence 5, Appl
157	12.6	43.4	36	2	US-08-558-107-7	Sequence 7, Appl	230	12.4	42.8	34	4	US-09-581-070-5	Sequence 5, Appl
158	12.6	43.4	36	2	US-09-423-539-7	Sequence 7, Appl	231	12.4	42.8	37	1	US-08-049-264C-55	Sequence 55, Appl
159	12.6	43.4	36	3	US-08-218-369-7	Sequence 7, Appl	232	12.4	42.8	37	1	US-08-476-562-55	Sequence 55, Appl
160	12.6	43.4	36	4	US-08-218-369-7	Sequence 7, Appl	233	12.4	42.8	37	1	US-08-479-723A-55	Sequence 55, Appl
161	12.6	43.4	36	4	US-08-218-369-15	Sequence 15, Appl	234	12.4	42.8	37	5	PCT-US94-04310-55	Sequence 54, Appl
162	12.6	43.4	36	4	US-09-904-599A-7	Sequence 7, Appl	235	12.4	42.8	38	4	US-09-371-772B-8446	Sequence 54, Appl
163	12.6	43.4	36	5	PCT-US95-03742-7	Sequence 7, Appl	236	12.4	42.8	44	1	US-08-049-264C-54	Sequence 54, Appl
164	12.6	43.4	36	5	PCT-US95-03742-7	Sequence 7, Appl	237	12.4	42.8	44	1	US-08-476-562-54	Sequence 54, Appl
165	12.6	43.4	36	5	PCT-US95-03742-15	Sequence 15, Appl	238	12.4	42.8	44	1	US-08-479-723A-54	Sequence 54, Appl
166	12.6	43.4	42	3	US-09-436-411-10	Sequence 10, Appl	239	12.4	42.8	44	5	PCT-US94-04310-54	Sequence 54, Appl
167	12.6	43.4	42	6	5281520-11	Patent No. 5281520	240	12.4	42.8	47	4	US-09-422-978-639	Sequence 3759, Ap
168	12.6	43.4	43	1	US-08-041-538-4	Sequence 4, Appl	241	12.4	42.8	47	4	US-05-623-326-37	Sequence 37, Appl
169	12.6	43.4	43	1	US-08-463-642-4	Sequence 4, Appl	242	12.4	42.8	48	4	US-09-443-199C-868	Sequence 868, App
170	12.6	43.4	43	1	US-08-455-602-4	Sequence 4, Appl	243	12.4	42.8	51	4	US-09-352-540A-4	Sequence 4, Appl
171	12.6	43.4	43	2	US-08-465-157-4	Sequence 4, Appl	244	12.4	42.8	65	4	US-09-799-645-4	Sequence 4, Appl
172	12.6	43.4	43	5	PCT-US91-09422-4	Sequence 4, Appl	245	12.4	42.8	65	4		
173	12.6	43.4	45	1	US-08-171-389-130	Sequence 130, App	246	12.4	42.8	65	4		

247	12.4	42.8	65	4	US-10-002-528-4	Sequence 4, Appl	Sequence 4, Appl	12.2	42.1	51	2	US-08-471-025-16	Sequence 16, Appl
248	12.4	42.8	68	4	US-08-356-171B-2762	Sequence 1762, Ap	Sequence 1762, Ap	12.2	42.1	51	3	US-08-473-446-39	Sequence 39, Appl
249	12.4	42.1	17	1	US-08-373-124A-1795	Sequence 1795, Ap	Sequence 1795, Ap	12.2	42.1	51	3	US-08-460-736-16	Sequence 16, Appl
250	12.2	42.1	17	1	US-08-435-628-1795	Sequence 1795, Ap	Sequence 1795, Ap	12.2	42.1	51	4	US-09-354-138-16	Sequence 16, Appl
251	12.2	42.1	17	4	US-09-827-998-281	Sequence 281, App	Sequence 281, App	12.2	42.1	51	4	US-09-535-370-16	Sequence 16, Appl
252	12.2	42.1	17	4	US-09-827-998-282	Sequence 282, App	Sequence 282, App	12.2	42.1	51	4	US-09-136-159A-16	Sequence 16, Appl
253	12.2	42.1	17	4	US-09-827-998-283	Sequence 283, App	Sequence 283, App	12.2	42.1	51	5	PCT-US96-00547-16	Sequence 16, Appl
254	12.2	42.1	19	3	US-08-532-896-53	Sequence 53, Appl	Sequence 53, Appl	12.2	42.1	51	6	PCT-US96-00547-16	Sequence 16, Appl
255	12.2	42.1	20	4	US-09-198-452A-6382	Sequence 6382, Ap	Sequence 6382, Ap	12.2	42.1	51	6	5514566-10	Patent No. 5514566
256	12.2	42.1	20	4	US-09-601-144-11	Sequence 11, Appl	Sequence 11, Appl	12.2	42.1	55	4	US-08-434-099A-17	Sequence 17, Appl
257	12.2	42.1	22	4	US-09-375-673B-42	Sequence 42, Appl	Sequence 42, Appl	12.2	42.1	58	4	US-09-621-976-12180	Sequence 12180, A
258	12.2	42.1	22	4	US-08-817-913-25	Sequence 25, Appl	Sequence 25, Appl	12.2	42.1	59	1	US-08-009-965-3	Sequence 3, Appl
259	12.2	42.1	25	4	US-09-887-637B-4	Sequence 4, Appl	Sequence 4, Appl	12.2	42.1	59	3	US-08-483-511-35	Sequence 35, Appl
260	12.2	42.1	25	4	US-09-827-998-1086	Sequence 1086, Ap	Sequence 1086, Ap	12.2	42.1	59	5	PCT-US91-01009-35	Sequence 35, Appl
261	12.2	42.1	25	4	US-09-827-998-1106	Sequence 1106, Ap	Sequence 1106, Ap	12.2	42.1	70	2	US-08-488-402A-127	Sequence 127, App
262	12.2	42.1	29	1	US-08-467-420A-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	70	2	US-08-488-402A-127	Sequence 127, App
263	12.2	42.1	29	1	US-08-470-110A-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	70	5	PCT-US96-09472-127	Sequence 127, App
264	12.2	42.1	29	1	US-08-667-769A-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	78	1	US-08-351-748-19	Sequence 19, Appl
265	12.2	42.1	29	1	US-08-940-371-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	78	1	US-08-430-536A-19	Sequence 19, Appl
266	12.2	42.1	29	2	US-08-483-636-30	Sequence 30, Appl	Sequence 30, Appl	12.2	42.1	78	2	US-08-684-547-19	Sequence 19, Appl
267	12.2	42.1	29	2	US-08-483-632-30	Sequence 30, Appl	Sequence 30, Appl	12.2	42.1	78	4	US-09-621-976-12398	Sequence 12398, A
268	12.2	42.1	29	3	US-08-637-647-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	78	5	PCT-US91-02246-19	Sequence 19, Appl
269	12.2	42.1	29	4	US-08-793-273C-19	Sequence 19, Appl	Sequence 19, Appl	12.2	42.1	80	1	US-07-832-905B-61	Sequence 61, Appl
270	12.2	42.1	29	4	US-09-304-232-323	Sequence 323, App	Sequence 323, App	12.2	42.1	80	1	US-07-832-905B-61	Sequence 62, Appl
271	12.2	42.1	29	5	PCT-US94-07659-13	Sequence 13, Appl	Sequence 13, Appl	12.2	42.1	80	2	US-08-700-757-61	Sequence 61, Appl
272	12.2	42.1	29	5	PCT-US95-11684-19	Sequence 19, Appl	Sequence 19, Appl	12.2	42.1	80	2	US-08-700-757-61	Sequence 62, Appl
273	12.2	42.1	29	5	PCT-US95-1708A-22	Sequence 22, Appl	Sequence 22, Appl	12.2	42.1	80	2	US-08-860-882A-43	Sequence 43, Appl
274	12.2	42.1	30	1	US-08-479-487-43	Sequence 43, Appl	Sequence 43, Appl	12.2	42.1	80	4	US-09-011-769A-10	Sequence 10, Appl
275	12.2	42.1	30	1	US-08-479-487-55	Sequence 55, Appl	Sequence 55, Appl	12.2	42.1	80	4	US-09-166-186-198	Sequence 198, App
276	12.2	42.1	30	3	US-08-854-170-3	Sequence 3, Appl	Sequence 3, Appl	12.2	42.1	20	3	US-09-333-932-198	Sequence 198, App
277	12.2	42.1	30	3	US-08-813-842-47	Sequence 47, Appl	Sequence 47, Appl	12.2	42.1	20	3	US-09-333-932-198	Sequence 198, App
278	12.2	42.1	30	4	US-09-898-627-2	Sequence 2, Appl	Sequence 2, Appl	12.2	42.1	21	3	US-09-333-932-198	Sequence 12, Appl
279	12.2	42.1	32	3	US-09-295-028-77	Sequence 77, Appl	Sequence 77, Appl	12.2	42.1	21	4	US-09-422-978-6777	Sequence 6777, Ap
280	12.2	42.1	32	3	US-09-295-028-77	Sequence 77, Appl	Sequence 77, Appl	12.2	42.1	22	4	US-09-375-673B-49	Sequence 49, Appl
281	12.2	42.1	32	4	US-09-692-064-8	Sequence 8, Appl	Sequence 8, Appl	12.2	42.1	22	4	US-09-375-673B-51	Sequence 51, Appl
282	12.2	42.1	32	4	US-09-692-064-8	Sequence 8, Appl	Sequence 8, Appl	12.2	42.1	22	4	US-09-375-673B-51	Sequence 51, Appl
283	12.2	42.1	33	3	US-09-693-542-77	Sequence 77, Appl	Sequence 77, Appl	12.2	42.1	33	1	US-07-714-687-55	Sequence 55, Appl
284	12.2	42.1	34	6	US-07-861-458C-59	Sequence 59, Appl	Sequence 59, Appl	12.2	42.1	33	1	US-08-224-331-54	Sequence 54, Appl
285	12.2	42.1	36	2	US-07-756-251A-6	Sequence 6, Appl	Sequence 6, Appl	12.2	42.1	33	1	US-08-484-304-54	Sequence 54, Appl
286	12.2	42.1	36	2	US-08-696-566-7	Sequence 7, Appl	Sequence 7, Appl	12.2	42.1	34	2	US-08-484-304-54	Sequence 104, App
287	12.2	42.1	36	3	US-08-911-860-7	Sequence 7, Appl	Sequence 7, Appl	12.2	42.1	35	1	US-08-102-567-17	Sequence 17, Appl
288	12.2	42.1	38	1	US-08-373-124A-809	Sequence 809, App	Sequence 809, App	12.2	42.1	35	3	US-08-102-567-17	Sequence 17, Appl
289	12.2	42.1	38	1	US-08-373-124A-809	Sequence 809, App	Sequence 809, App	12.2	42.1	35	3	US-08-462-947-17	Sequence 55, Appl
290	12.2	42.1	38	1	US-08-373-124A-877	Sequence 877, App	Sequence 877, App	12.2	42.1	37	1	US-07-714-687-55	Sequence 55, Appl
291	12.2	42.1	38	1	US-08-373-124A-1328	Sequence 1328, Ap	Sequence 1328, Ap	12.2	42.1	37	1	US-08-224-331-55	Sequence 55, Appl
292	12.2	42.1	38	1	US-08-435-628-303	Sequence 303, App	Sequence 303, App	12.2	42.1	37	1	US-08-484-304-55	Sequence 55, Appl
293	12.2	42.1	38	1	US-08-435-628-809	Sequence 809, App	Sequence 809, App	12.2	42.1	37	1	US-08-484-304-55	Sequence 55, Appl
294	12.2	42.1	38	1	US-08-435-628-877	Sequence 877, App	Sequence 877, App	12.2	42.1	40	3	US-09-306-290-16	Sequence 16, Appl
295	12.2	42.1	38	1	US-08-435-628-877	Sequence 877, App	Sequence 877, App	12.2	42.1	40	3	US-09-306-290-16	Sequence 16, App
296	12.2	42.1	38	1	US-08-435-628-1328	Sequence 1328, Ap	Sequence 1328, Ap	12.2	42.1	41	4	US-08-280-116-146	Sequence 146, App
297	12.2	42.1	39	6	5519127-34	Patent No. 5519127	Patent No. 5519127	12.2	42.1	41	4	US-08-464-083-3	Sequence 3, Appl
298	12.2	42.1	40	4	US-09-294-584A-4	Sequence 4, Appl	Sequence 4, Appl	12.2	42.1	47	1	US-08-443-965B-5	Sequence 5, Appl
299	12.2	42.1	40	4	US-08-833-814A-6	Sequence 6, Appl	Sequence 6, Appl	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
300	12.2	42.1	42	3	US-08-434-099A-16	Sequence 16, Appl	Sequence 16, Appl	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
301	12.2	42.1	44	1	US-07-832-905B-58	Sequence 58, Appl	Sequence 58, Appl	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
302	12.2	42.1	44	2	US-08-700-757-58	Sequence 58, Appl	Sequence 58, Appl	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
303	12.2	42.1	45	3	US-08-860-882A-19	Sequence 19, Appl	Sequence 19, Appl	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
304	12.2	42.1	45	3	US-08-997-918-10	Sequence 10, Appl	Sequence 10, Appl	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
305	12.2	42.1	45	3	US-08-997-918-24	Sequence 24, Appl	Sequence 24, Appl	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
306	12.2	42.1	47	4	US-09-011-769A-15	Sequence 15, Appl	Sequence 15, Appl	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
307	12.2	42.1	47	4	US-09-641-638-1000	Sequence 1000, Ap	Sequence 1000, Ap	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
308	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
309	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
310	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
311	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
312	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
313	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
314	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
315	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
316	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
317	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
318	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl
319	12.2	42.1	47	4	US-09-671-317-500	Sequence 500, App	Sequence 500, App	12.2	42.1	47	2	US-08-443-965B-5	Sequence 5, Appl

393	12	41.4	80	1	US-08-469-557-21	Sequence 21, Appl	C 466	11.8	40.7	47	4	US-09-641-638-852	Sequence 852, App
394	12	41.4	80	2	US-08-290-793B-21	Sequence 21, Appl	C 467	11.8	40.7	47	4	US-09-671-317-839	Sequence 829, App
C 395	11.8	40.7	17	4	US-09-827-998-284	Sequence 284, App	C 468	11.8	40.7	47	4	US-09-422-978-787	Sequence 734, App
C 396	11.8	40.7	17	4	US-09-827-998-285	Sequence 285, App	C 469	11.8	40.7	47	4	US-09-422-978-2486	Sequence 2486, App
C 397	11.8	40.7	20	4	US-09-091-952A-91	Sequence 91, Appl	C 470	11.8	40.7	47	4	US-09-422-978-2594	Sequence 2594, App
C 398	11.8	40.7	24	2	US-08-451-822A-11	Sequence 11, Appl	C 471	11.8	40.7	48	4	US-09-892-188B-12	Sequence 12, Appl
C 399	11.8	40.7	24	2	US-08-323-430-11	Sequence 11, Appl	C 472	11.8	40.7	54	1	US-08-073-963-3	Sequence 3, Appl
C 400	11.8	40.7	25	4	US-09-827-998-1107	Sequence 1107, App	C 473	11.8	40.7	54	1	US-08-073-963-4	Sequence 4, Appl
C 401	11.8	40.7	26	1	US-09-827-998-1108	Sequence 1108, App	C 474	11.8	40.7	54	1	US-08-487-412-3	Sequence 3, Appl
C 402	11.8	40.7	26	1	US-08-599-252-43	Sequence 43, Appl	C 475	11.8	40.7	54	1	US-08-487-412-4	Sequence 4, Appl
C 403	11.8	40.7	26	5	PCT-US96-06352-43	Sequence 43, Appl	C 476	11.8	40.7	54	2	US-08-418-848A-57	Sequence 57, Appl
C 404	11.8	40.7	26	5	PCT-US96-06353-43	Sequence 43, Appl	C 477	11.8	40.7	54	4	US-08-584-040-2949	Sequence 2949, App
C 405	11.8	40.7	27	6	5258283-10	Patent No. 5258283	C 478	11.8	40.7	54	4	US-08-706-945D-105	Sequence 105, App
C 406	11.8	40.7	29	1	US-08-531-556-99	Sequence 99, Appl	C 479	11.8	40.7	54	4	US-09-371-772B-8615	Sequence 8615, App
C 407	11.8	40.7	29	2	US-08-690-73A-30	Sequence 30, Appl	C 480	11.8	40.7	54	6	5459046-8	Patent No. 5459046
C 408	11.8	40.7	29	3	US-08-742-185-30	Sequence 30, Appl	C 481	11.8	40.7	57	4	US-09-318-786-7	Sequence 7, Appl
C 409	11.8	40.7	30	1	US-08-381-280-24	Sequence 24, Appl	C 482	11.8	40.7	60	3	US-08-478-097A-32	Sequence 32, Appl
C 410	11.8	40.7	30	2	US-08-445-533-24	Sequence 24, Appl	C 483	11.8	40.7	60	3	US-09-496-398-32	Sequence 32, Appl
C 411	11.8	40.7	30	3	US-09-052-085-24	Sequence 24, Appl	C 484	11.8	40.7	61	3	US-08-952-793-362	Sequence 362, App
C 412	11.8	40.7	31	4	US-09-063-733A-20	Sequence 20, Appl	C 485	11.8	40.7	61	4	US-09-849-928-362	Sequence 362, App
C 413	11.8	40.7	31	4	US-09-429-693-3	Sequence 3, Appl	C 486	11.8	40.7	61	5	PCT-US96-09455A-362	Sequence 362, App
C 414	11.8	40.7	32	2	US-08-867-941-60	Sequence 60, Appl	C 487	11.8	40.7	62	1	US-08-206-384-7	Sequence 7, Appl
C 415	11.8	40.7	32	3	US-09-074-658-60	Sequence 60, Appl	C 488	11.8	40.7	62	3	US-08-752-722-7	Sequence 7, Appl
C 416	11.8	40.7	32	4	US-09-230-288-13	Sequence 13, Appl	C 489	11.8	40.7	63	3	US-09-237-712-68	Sequence 68, Appl
C 417	11.8	40.7	34	3	US-08-544-381B-174	Sequence 174, App	C 490	11.8	40.7	64	4	US-09-059-625-17	Sequence 17, Appl
C 418	11.8	40.7	36	1	US-08-319-492B-234	Sequence 234, App	C 491	11.8	40.7	66	3	US-09-237-712-64	Sequence 64, Appl
C 419	11.8	40.7	36	1	US-08-319-492B-581	Sequence 581, App	C 492	11.8	40.7	68	4	US-09-193-612B-13	Sequence 13, Appl
C 420	11.8	40.7	36	1	US-08-363-240A-924	Sequence 924, App	C 493	11.8	40.7	70	4	US-09-647-036A-6	Sequence 6, Appl
C 421	11.8	40.7	36	2	US-08-292-620A-918	Sequence 918, App	C 494	11.8	40.7	72	3	US-08-950-961-23	Sequence 23, Appl
C 422	11.8	40.7	36	2	US-08-585-684B-327	Sequence 327, App	C 495	11.8	40.7	72	4	US-09-479-776-23	Sequence 23, Appl
C 423	11.8	40.7	36	2	US-08-585-684B-2044	Sequence 2044, App	C 496	11.8	40.0	20	4	US-09-488-856A-29	Sequence 29, Appl
C 424	11.8	40.7	36	2	US-08-585-684B-2385	Sequence 2385, App	C 497	11.8	40.0	20	4	US-09-488-856A-29	Sequence 29, Appl
C 425	11.8	40.7	36	2	US-08-585-684B-2386	Sequence 2386, App	C 498	11.8	40.0	20	4	US-09-488-856A-29	Sequence 29, Appl
C 426	11.8	40.7	36	3	US-09-071-845-918	Sequence 918, App	C 499	11.8	40.0	21	4	US-09-422-978-10520	Sequence 10520, A
C 427	11.8	40.7	36	3	US-09-440-001-3	Sequence 3, Appl	C 500	11.8	40.0	24	2	US-08-507-634-5	Sequence 5, Appl
C 428	11.8	40.7	36	3	US-09-038-073-327	Sequence 327, App	C 501	11.8	40.0	24	3	PCT-US95-12608-25	Sequence 25, Appl
C 429	11.8	40.7	36	3	US-09-038-073-2044	Sequence 2044, App	C 502	11.8	40.0	24	5	PCT-US95-12608-25	Sequence 25, Appl
C 430	11.8	40.7	36	3	US-09-038-073-2385	Sequence 2385, App	C 503	11.8	40.0	25	3	US-08-891-789B-32	Sequence 32, Appl
C 431	11.8	40.7	36	3	US-09-038-073-2386	Sequence 2386, App	C 504	11.8	40.0	25	3	US-09-601-258-7	Sequence 7, Appl
C 432	11.8	40.7	36	3	US-08-793-634B-18	Sequence 18, Appl	C 505	11.8	40.0	26	1	US-08-154-019-5	Sequence 5, Appl
C 433	11.8	40.7	36	4	US-09-374-962-19	Sequence 19, Appl	C 506	11.8	40.0	26	1	US-08-154-019-12	Sequence 12, Appl
C 434	11.8	40.7	36	4	US-09-605-685-3	Sequence 3, Appl	C 507	11.8	40.0	26	1	US-08-461-333-5	Sequence 5, Appl
C 435	11.8	40.7	37	4	US-08-705-477E-59	Sequence 59, Appl	C 508	11.8	40.0	26	3	US-08-464-167-12	Sequence 12, Appl
C 436	11.8	40.7	38	1	US-08-373-124A-545	Sequence 545, App	C 509	11.8	40.0	26	3	US-08-464-167-12	Sequence 12, Appl
C 437	11.8	40.7	38	1	US-08-373-124A-577	Sequence 577, App	C 510	11.8	40.0	26	3	US-09-158-313-5	Sequence 5, Appl
C 438	11.8	40.7	38	1	US-08-373-124A-1199	Sequence 1199, App	C 511	11.8	40.0	26	3	US-09-158-313-5	Sequence 5, Appl
C 439	11.8	40.7	38	1	US-08-373-124A-1306	Sequence 1306, App	C 512	11.8	40.0	26	3	US-08-476-798-5	Sequence 12, Appl
C 440	11.8	40.7	38	1	US-08-373-124A-1584	Sequence 1584, App	C 513	11.8	40.0	26	3	US-08-476-798-5	Sequence 12, Appl
C 441	11.8	40.7	38	1	US-08-373-124A-2326	Sequence 2326, App	C 514	11.8	40.0	26	4	US-09-689-255C-6	Sequence 6, Appl
C 442	11.8	40.7	38	1	US-08-373-124A-2432	Sequence 2432, App	C 515	11.8	40.0	28	4	US-09-438-954-21	Sequence 21, Appl
C 443	11.8	40.7	38	1	US-08-373-124A-2508	Sequence 2508, App	C 516	11.8	40.0	29	4	US-09-304-232-345	Sequence 345, App
C 444	11.8	40.7	38	1	US-08-373-124A-2584	Sequence 2584, App	C 517	11.8	40.0	30	4	US-09-937-832-21	Sequence 21, Appl
C 445	11.8	40.7	38	1	US-08-435-628-545	Sequence 545, App	C 518	11.8	40.0	31	2	US-08-347-563A-35	Sequence 35, Appl
C 446	11.8	40.7	38	1	US-08-435-628-577	Sequence 577, App	C 519	11.8	40.0	31	3	US-08-485-942A-35	Sequence 35, Appl
C 447	11.8	40.7	38	1	US-08-435-628-1199	Sequence 1199, App	C 520	11.8	40.0	31	3	US-08-485-942A-35	Sequence 35, Appl
C 448	11.8	40.7	38	1	US-08-435-628-1306	Sequence 1306, App	C 521	11.8	40.0	31	3	US-08-488-208A-35	Sequence 35, Appl
C 449	11.8	40.7	38	1	US-08-435-628-1594	Sequence 1594, App	C 522	11.8	40.0	31	4	US-08-483-211A-35	Sequence 35, Appl
C 450	11.8	40.7	38	1	US-08-435-628-2326	Sequence 2326, App	C 523	11.8	40.0	31	4	US-08-488-223A-35	Sequence 35, Appl
C 451	11.8	40.7	38	1	US-08-435-628-2432	Sequence 2432, App	C 524	11.8	40.0	31	4	US-08-438-431A-35	Sequence 35, Appl
C 452	11.8	40.7	38	1	US-08-435-628-2508	Sequence 2508, App	C 525	11.8	40.0	31	4	US-08-488-225A-35	Sequence 35, Appl
C 453	11.8	40.7	38	1	US-08-435-628-2584	Sequence 2584, App	C 526	11.8	40.0	32	2	US-08-959-998-407	Sequence 407, App
C 454	11.8	40.7	38	4	US-09-325-554-10	Sequence 10, Appl	C 527	11.8	40.0	32	4	US-09-225-928-407	Sequence 407, App
C 455	11.8	40.7	38	4	US-09-325-554-11	Sequence 11, Appl	C 528	11.8	40.0	32	4	US-09-225-928-407	Sequence 407, App
C 456	11.8	40.7	38	4	US-09-371-772B-7942	Sequence 7942, App	C 529	11.8	40.0	32	4	US-08-979-847B-104	Sequence 104, App
C 457	11.8	40.7	38	4	US-08-679-645-24	Sequence 24, Appl	C 530	11.8	40.0	34	4	US-09-663-733A-52	Sequence 52, Appl
C 458	11.8	40.7	42	4	US-08-832-65	Sequence 65, Appl	C 531	11.8	40.0	34	4	US-08-488-446-612	Sequence 612, App
C 459	11.8	40.7	43	3	US-09-422-978-3434	Sequence 3434, App	C 532	11.8	40.0	34	4	US-08-467-344A-612	Sequence 612, App
C 460	11.8	40.7	43	4	US-09-820-923B-65	Sequence 65, Appl	C 533	11.8	40.0	34	4	US-08-467-344A-612	Sequence 612, App
C 461	11.8	40.7	44	2	US-08-343-443B-39	Sequence 39, Appl	C 534	11.8	40.0	35	6	542260-12	Patent No. 542260
C 462	11.8	40.7	44	2	US-07-832-905B-59	Sequence 59, Appl	C 535	11.8	40.0	36	4	US-09-746-359A-42	Sequence 42, Appl
C 463	11.8	40.7	47	1	US-07-832-905B-59	Sequence 59, Appl	C 536	11.8	40.0	36	4	US-09-593-580B-29	Sequence 29, Appl
C 464	11.8	40.7	47	2	US-08-700-757-59	Sequence 59, Appl	C 537	11.8	40.0	37	1	US-07-598-737C-5	Sequence 5, Appl
C 465	11.8	40.7	47	4	US-09-641-638-663	Sequence 663, App	C 538	11.8	40.0	37	1	US-08-084-718-18	Sequence 18, Appl

539	11.6	40.0	37	1	US-08-443-976-18	Sequence 18, Appl	Sequence 18, Appl	c 612	11.6	40.0	66	4	US-08-956-171B-1643	Sequence 1643, Ap
540	11.6	40.0	37	1	US-08-443-977-18	Sequence 18, Appl	Sequence 18, Appl	c 613	11.6	40.0	69	3	US-08-832-985-14	Sequence 14, Appl
541	11.6	40.0	37	3	US-08-721-458B-59	Sequence 59, Appl	Sequence 59, Appl	c 614	11.6	40.0	69	4	US-09-410-903-95	Sequence 95, Appl
542	11.6	40.0	38	1	US-08-390-850-840	Sequence 840, App	Sequence 840, App	c 615	11.6	40.0	69	4	US-08-835-159-14	Sequence 14, Appl
543	11.6	40.0	38	1	US-08-390-850-862	Sequence 862, App	Sequence 862, App	c 616	11.6	40.0	69	4	US-09-621-976-16527	Sequence 16527, A
544	11.6	40.0	38	1	US-08-390-850-897	Sequence 897, App	Sequence 897, App	c 617	11.6	40.0	70	3	US-09-364-380-11	Sequence 11, Appl
545	11.6	40.0	38	1	US-08-373-124A-453	Sequence 453, App	Sequence 453, App	c 618	11.6	40.0	71	3	US-09-275-850-143	Sequence 143, App
546	11.6	40.0	38	1	US-08-373-124A-591	Sequence 591, App	Sequence 591, App	c 619	11.6	40.0	75	3	US-08-952-457-6	Sequence 6, Appli
547	11.6	40.0	38	1	US-08-373-124A-1426	Sequence 1426, Ap	Sequence 1426, Ap	c 620	11.6	40.0	75	4	US-09-025-769B-311	Sequence 311, App
548	11.6	40.0	38	1	US-08-373-124A-1500	Sequence 1500, Ap	Sequence 1500, Ap	c 621	11.6	40.0	76	1	US-07-593-657-10	Sequence 10, Appl
549	11.6	40.0	38	1	US-08-435-634-840	Sequence 840, App	Sequence 840, App	c 622	11.6	40.0	76	4	US-09-025-769B-310	Sequence 310, App
550	11.6	40.0	38	1	US-08-435-634-862	Sequence 862, App	Sequence 862, App	c 623	11.6	40.0	76	4	US-09-963-137-32	Sequence 32, Appl
551	11.6	40.0	38	1	US-08-435-634-897	Sequence 897, App	Sequence 897, App	c 624	11.4	39.3	14	3	US-08-847-844A-99	Sequence 99, Appl
552	11.6	40.0	38	1	US-08-435-628-453	Sequence 453, App	Sequence 453, App	c 625	11.4	39.3	17	4	US-08-584-040-3752	Sequence 3752, Ap
553	11.6	40.0	38	1	US-08-435-628-591	Sequence 591, App	Sequence 591, App	c 626	11.4	39.3	17	4	US-08-371-772B-1519	Sequence 1519, Ap
554	11.6	40.0	38	1	US-08-435-628-1426	Sequence 1426, Ap	Sequence 1426, Ap	c 627	11.4	39.3	17	4	US-08-371-772B-619	Sequence 619, Ap
555	11.6	40.0	38	1	US-08-435-628-1500	Sequence 1500, Ap	Sequence 1500, Ap	c 628	11.4	39.3	21	2	US-08-117-952-169	Sequence 169, App
556	11.6	40.0	38	1	US-08-469-260A-611	Sequence 611, App	Sequence 611, App	c 629	11.4	39.3	21	4	US-08-745-995A-37	Sequence 37, Appl
557	11.6	40.0	38	4	US-08-469-260A-623	Sequence 623, App	Sequence 623, App	c 630	11.4	39.3	21	4	US-09-005-352-37	Sequence 37, Appl
558	11.6	40.0	38	4	US-08-488-446-611	Sequence 611, App	Sequence 611, App	c 631	11.4	39.3	22	4	US-09-375-673B-52	Sequence 52, Appl
559	11.6	40.0	38	4	US-08-488-446-623	Sequence 623, App	Sequence 623, App	c 632	11.4	39.3	24	3	US-09-253-025-53	Sequence 53, Appl
560	11.6	40.0	38	4	US-08-467-344A-611	Sequence 611, App	Sequence 611, App	c 633	11.4	39.3	24	4	US-09-356-806-82	Sequence 82, Appl
561	11.6	40.0	38	4	US-08-467-344A-623	Sequence 623, App	Sequence 623, App	c 634	11.4	39.3	24	4	US-09-784-188B-53	Sequence 53, Appl
562	11.6	40.0	40	3	US-09-306-290-34	Sequence 34, Appl	Sequence 34, Appl	c 635	11.4	39.3	25	1	US-07-842-089E-38	Sequence 38, Appl
563	11.6	40.0	41	1	US-07-931-473B-63	Sequence 63, Appl	Sequence 63, Appl	c 636	11.4	39.3	25	1	US-08-264-485-38	Sequence 38, Appl
564	11.6	40.0	41	1	US-07-931-473B-87	Sequence 87, Appl	Sequence 87, Appl	c 637	11.4	39.3	25	2	US-08-690-734A-54	Sequence 54, Appl
565	11.6	40.0	41	1	US-07-714-131C-63	Sequence 63, Appl	Sequence 63, Appl	c 638	11.4	39.3	25	3	US-08-742-185-54	Sequence 54, Appl
566	11.6	40.0	41	1	US-07-714-131C-87	Sequence 87, Appl	Sequence 87, Appl	c 639	11.4	39.3	25	4	US-09-027-287-22	Sequence 22, Appl
567	11.6	40.0	41	1	US-08-412-110-63	Sequence 63, Appl	Sequence 63, Appl	c 640	11.4	39.3	25	4	US-09-252-656B-22	Sequence 22, Appl
568	11.6	40.0	41	1	US-08-412-110-87	Sequence 87, Appl	Sequence 87, Appl	c 641	11.4	39.3	26	2	US-08-533-323-22	Sequence 22, Appl
569	11.6	40.0	41	1	US-08-409-442A-63	Sequence 63, Appl	Sequence 63, Appl	c 642	11.4	39.3	26	2	US-08-639-857-9	Sequence 9, Appli
570	11.6	40.0	41	1	US-08-409-442A-87	Sequence 87, Appl	Sequence 87, Appl	c 643	11.4	39.3	27	1	US-08-758-306-904	Sequence 904, App
571	11.6	40.0	41	1	US-08-409-442A-356	Sequence 356, App	Sequence 356, App	c 644	11.4	39.3	27	4	US-08-584-040-6545	Sequence 6545, Ap
572	11.6	40.0	41	2	US-08-469-609A-63	Sequence 63, Appl	Sequence 63, Appl	c 645	11.4	39.3	27	5	PCT-US93-09070-13	Sequence 13, Appl
573	11.6	40.0	41	2	US-08-469-609A-87	Sequence 87, Appl	Sequence 87, Appl	c 646	11.4	39.3	28	1	US-08-220-606B-31	Sequence 31, Appl
574	11.6	40.0	41	2	US-08-469-609A-356	Sequence 356, App	Sequence 356, App	c 647	11.4	39.3	29	1	US-08-230-606B-32	Sequence 32, Appl
575	11.6	40.0	41	3	US-09-143-190-63	Sequence 63, Appl	Sequence 63, Appl	c 648	11.4	39.3	29	1	US-08-586-024-1	Sequence 1, Appli
576	11.6	40.0	41	3	US-09-143-190-87	Sequence 87, Appl	Sequence 87, Appl	c 649	11.4	39.3	29	3	US-09-020-818-1	Sequence 1, Appli
577	11.6	40.0	41	3	US-09-143-190-356	Sequence 356, App	Sequence 356, App	c 650	11.4	39.3	29	3	US-08-907-740-1	Sequence 1, Appli
578	11.6	40.0	41	4	US-09-502-344-63	Sequence 63, Appl	Sequence 63, Appl	c 651	11.4	39.3	29	4	US-09-797-467-1	Sequence 1, Appli
579	11.6	40.0	41	4	US-09-502-344-87	Sequence 87, Appl	Sequence 87, Appl	c 652	11.4	39.3	30	1	US-08-381-280-26	Sequence 26, Appl
580	11.6	40.0	41	4	US-09-502-344-356	Sequence 356, App	Sequence 356, App	c 653	11.4	39.3	30	1	US-08-453-924-11	Sequence 11, Appl
581	11.6	40.0	41	4	US-09-551-656-55	Sequence 55, Appl	Sequence 55, Appl	c 654	11.4	39.3	30	2	US-08-445-533-26	Sequence 26, Appl
582	11.6	40.0	41	4	US-09-650-855-55	Sequence 55, Appl	Sequence 55, Appl	c 655	11.4	39.3	30	3	US-09-052-085-26	Sequence 26, Appl
583	11.6	40.0	43	4	US-09-434-354-4	Sequence 4, Appli	Sequence 4, Appli	c 656	11.4	39.3	32	1	US-08-299-810A-17	Sequence 17, Appl
584	11.6	40.0	45	3	US-08-721-458B-62	Sequence 62, Appl	Sequence 62, Appl	c 657	11.4	39.3	32	1	US-08-299-810A-18	Sequence 18, Appl
585	11.6	40.0	46	1	US-08-794-153-5	Sequence 5, Appli	Sequence 5, Appli	c 658	11.4	39.3	32	1	US-08-299-810A-20	Sequence 20, Appl
586	11.6	40.0	46	1	US-09-115-566-5	Sequence 5, Appli	Sequence 5, Appli	c 659	11.4	39.3	32	2	US-08-599-602-15	Sequence 15, Appl
587	11.6	40.0	46	3	US-09-478-189-125	Sequence 125, App	Sequence 125, App	c 660	11.4	39.3	32	2	US-08-544-381B-173	Sequence 173, App
588	11.6	40.0	47	1	US-08-399-696-26	Sequence 988, App	Sequence 988, App	c 661	11.4	39.3	32	3	US-09-197-816-15	Sequence 15, Appl
589	11.6	40.0	47	1	US-09-422-978-988	Sequence 1021, Ap	Sequence 1021, Ap	c 662	11.4	39.3	33	4	US-08-387-805-3	Sequence 3, Appli
590	11.6	40.0	47	4	US-09-422-978-1021	Sequence 1076, Ap	Sequence 1076, Ap	c 663	11.4	39.3	33	4	US-09-075-019-12	Sequence 12, Appl
591	11.6	40.0	47	4	US-09-422-978-1076	Sequence 1093, Ap	Sequence 1093, Ap	c 664	11.4	39.3	34	3	US-08-470-535-18	Sequence 18, Appl
592	11.6	40.0	47	4	US-09-422-978-1093	Sequence 1513, Ap	Sequence 1513, Ap	c 665	11.4	39.3	36	3	US-08-250-802-8	Sequence 8, Appli
593	11.6	40.0	47	4	US-09-422-978-1513	Sequence 1806, Ap	Sequence 1806, Ap	c 666	11.4	39.3	36	3	US-08-469-260A-631	Sequence 631, App
594	11.6	40.0	47	4	US-09-422-978-1806	Sequence 3054, Ap	Sequence 3054, Ap	c 667	11.4	39.3	36	4	US-08-488-446-631	Sequence 631, App
595	11.6	40.0	47	4	US-09-422-978-3054	Sequence 3129, Ap	Sequence 3129, Ap	c 668	11.4	39.3	36	4	US-08-487-344A-631	Sequence 631, App
596	11.6	40.0	47	4	US-09-422-978-3129	Sequence 122, App	Sequence 122, App	c 669	11.4	39.3	36	4	US-09-643-217-8	Sequence 8, Appli
597	11.6	40.0	50	3	US-09-388-972-122	Sequence 21, Appl	Sequence 21, Appl	c 670	11.4	39.3	37	1	US-08-741-881-106	Sequence 106, App
598	11.6	40.0	50	4	US-09-383-316-21	Sequence 18, Appl	Sequence 18, Appl	c 671	11.4	39.3	37	1	US-08-739-158-106	Sequence 106, App
599	11.6	40.0	50	4	US-08-956-171B-1996	Sequence 1996, Ap	Sequence 1996, Ap	c 672	11.4	39.3	37	2	US-08-739-167-106	Sequence 106, App
600	11.6	40.0	51	4	US-09-443-199C-18	Sequence 854, App	Sequence 854, App	c 673	11.4	39.3	37	2	US-08-404-796-106	Sequence 106, App
601	11.6	40.0	51	4	US-09-443-199C-854	Sequence 287, App	Sequence 287, App	c 674	11.4	39.3	37	3	US-08-931-869-106	Sequence 106, App
602	11.6	40.0	51	4	US-09-275-850-287	Sequence 5102, App	Sequence 5102, App	c 675	11.4	39.3	37	3	US-09-350-399-106	Sequence 106, App
603	11.6	40.0	53	3	US-08-956-171B-5102	Sequence 45, Appl	Sequence 45, Appl	c 676	11.4	39.3	37	4	US-09-236-140A-106	Sequence 106, App
604	11.6	40.0	58	4	US-09-619-213B-45	Sequence 46, Appl	Sequence 46, Appl	c 677	11.4	39.3	38	1	US-08-104-072B-34	Sequence 34, Appl
605	11.6	40.0	61	1	US-08-084-718-46	Sequence 46, Appl	Sequence 46, Appl	c 678	11.4	39.3	38	1	US-09-371-772B-7874	Sequence 7874, Ap
606	11.6	40.0	63	1	US-08-443-976-46	Sequence 46, Appl	Sequence 46, Appl	c 679	11.4	39.3	38	4	US-09-371-772B-8215	Sequence 8215, Ap
607	11.6	40.0	63	1	US-08-443-976-46	Sequence 46, Appl	Sequence 46, Appl	c 680	11.4	39.3	38	4	US-09-371-772B-11756	Sequence 11756, A
608	11.6	40.0	63	1	US-08-443-976-46	Sequence 47, Appl	Sequence 47, Appl	c 681	11.4	39.3	38	4	US-09-371-772B-12340	Sequence 12340, A
609	11.6	40.0	65	1	US-08-084-718-47	Sequence 47, Appl	Sequence 47, Appl	c 682	11.4	39.3	38	4	US-09-371-772B-12499	Sequence 12499, A
610	11.6	40.0	65	1	US-08-443-976-47	Sequence 47, Appl	Sequence 47, Appl	c 683	11.4	39.3	38	4	US-09-371-772B-12520	Sequence 12520, A
611	11.6	40.0	65	1	US-08-443-977-47	Sequence 47, Appl	Sequence 47, Appl	c 684	11.4	39.3	38	4		

C 685	11.4	39.3	38	4	US-09-371-772B-12645	Sequence 12645, A	C 758	11.2	38.6	20	4	US-09-980-052-85	Sequence 85, Appl
C 686	11.4	39.3	40	4	US-09-731-466-1	Sequence 1, Appl	759	11.2	38.6	21	2	US-08-253-877C-65	Sequence 65, Appl
C 687	11.4	39.3	40	4	US-09-548-797B-170	Sequence 170, App	760	11.2	38.6	21	2	US-08-452-164A-65	Sequence 65, Appl
C 688	11.4	39.3	41	1	US-08-306-255-3	Sequence 4, Appl	761	11.2	38.6	22	4	US-09-159-871-10	Sequence 10, Appl
C 689	11.4	39.3	41	5	PCT-US93-09070-4	Sequence 4, Appl	762	11.2	38.6	22	4	US-09-375-673B-56	Sequence 56, Appl
C 690	11.4	39.3	44	1	US-10-113-842B-69	Sequence 69, Appl	C 763	11.2	38.6	23	2	US-08-747-536-28	Sequence 28, Appl
C 691	11.4	39.3	44	1	US-08-448-744-9	Sequence 9, Appl	764	11.2	38.6	24	2	US-08-332-766A-99	Sequence 99, Appl
C 692	11.4	39.3	45	1	US-08-641-638-833	Sequence 833, App	765	11.2	38.6	25	3	US-08-933-983-33	Sequence 33, Appl
C 693	11.4	39.3	46	4	US-09-338-907-231	Sequence 231, App	766	11.2	38.6	25	2	US-07-771-032P-7	Sequence 7, Appl
C 694	11.4	39.3	47	3	US-09-218-207-231	Sequence 231, App	C 767	11.2	38.6	25	2	US-08-257-781-5	Sequence 5, Appl
C 695	11.4	39.3	47	4	US-09-641-638-705	Sequence 705, App	768	11.2	38.6	25	2	US-08-827-998-1095	Sequence 1095, Ap
C 696	11.4	39.3	47	4	US-09-641-638-1034	Sequence 1034, Ap	C 769	11.2	38.6	25	4	US-09-866-108A-3196	Sequence 3196, Ap
C 697	11.4	39.3	47	4	US-09-641-638-1090	Sequence 1090, Ap	770	11.2	38.6	25	4	US-09-866-108A-3197	Sequence 3197, Ap
C 698	11.4	39.3	47	4	US-09-671-317-514	Sequence 514, App	771	11.2	38.6	25	5	PCT-US95-06857-5	Sequence 5, Appl
C 699	11.4	39.3	47	4	US-09-671-317-935	Sequence 935, App	C 772	11.2	38.6	25	5	PCT-US95-06857-5	Sequence 5, Appl
C 700	11.4	39.3	47	4	US-09-422-978-75	Sequence 75, Appl	C 773	11.2	38.6	26	1	US-08-160-861-5	Sequence 5, Appl
C 701	11.4	39.3	47	4	US-09-422-978-355	Sequence 355, App	C 774	11.2	38.6	26	1	US-08-542-363-5	Sequence 5, Appl
C 702	11.4	39.3	47	4	US-09-422-978-382	Sequence 386, App	C 775	11.2	38.6	26	3	US-09-100-089-5	Sequence 5, Appl
C 703	11.4	39.3	47	4	US-09-422-978-1028	Sequence 1028, Ap	C 776	11.2	38.6	26	3	US-09-100-089-5	Sequence 5, Appl
C 704	11.4	39.3	47	4	US-09-422-978-1135	Sequence 1135, Ap	C 777	11.2	38.6	26	3	US-09-311-260-136	Sequence 136, App
C 705	11.4	39.3	47	4	US-09-422-978-2273	Sequence 2273, Ap	C 778	11.2	38.6	26	4	US-09-670-827-5	Sequence 5, Appl
C 706	11.4	39.3	47	4	US-09-422-978-2469	Sequence 2469, Ap	C 779	11.2	38.6	27	4	US-08-584-040-3514	Sequence 3514, Ap
C 707	11.4	39.3	47	4	US-09-422-978-2567	Sequence 2567, Ap	C 780	11.2	38.6	28	3	US-08-867-902P-8	Sequence 8, Appl
C 708	11.4	39.3	47	4	US-09-422-978-3197	Sequence 3197, Ap	C 781	11.2	38.6	30	1	US-08-182-530-4	Sequence 4, Appl
C 709	11.4	39.3	47	4	US-09-422-978-3582	Sequence 3582, Ap	C 782	11.2	38.6	30	1	US-08-527-097-3	Sequence 3, Appl
C 710	11.4	39.3	47	4	US-09-422-978-3715	Sequence 3715, Ap	C 783	11.2	38.6	30	1	US-08-050-058B-4	Sequence 4, Appl
C 711	11.4	39.3	48	1	US-08-119-773-13	Sequence 13, Appl	C 784	11.2	38.6	30	2	US-08-463-587A-4	Sequence 7, Appl
C 712	11.4	39.3	48	1	US-08-897-956A-31	Sequence 31, Appl	C 785	11.2	38.6	30	2	US-08-463-587A-4	Sequence 8, Appl
C 713	11.4	39.3	49	4	US-09-554-929-68	Sequence 68, Appl	C 786	11.2	38.6	30	2	US-08-441-871-8	Sequence 8, Appl
C 714	11.4	39.3	50	4	US-09-554-929-127	Sequence 127, App	C 787	11.2	38.6	30	2	US-08-629-001A-110	Sequence 110, App
C 715	11.4	39.3	50	4	US-09-554-929-127	Sequence 2301, Ap	C 788	11.2	38.6	30	3	US-08-923-854-4	Sequence 4, Appl
C 716	11.4	39.3	51	4	US-10-083-304-13	Sequence 13, Appl	C 789	11.2	38.6	30	3	US-08-642-274D-189	Sequence 189, App
C 717	11.4	39.3	51	3	US-08-911-894-63	Sequence 63, Appl	C 790	11.2	38.6	30	5	PCT-US91-03133-4	Sequence 4, Appl
C 718	11.4	39.3	56	4	US-09-724-916A-75	Sequence 75, Appl	C 791	11.2	38.6	31	1	US-08-390-850-236	Sequence 236, App
C 719	11.4	39.3	56	4	US-09-724-916A-76	Sequence 76, Appl	C 792	11.2	38.6	31	1	US-08-390-850-237	Sequence 237, App
C 720	11.4	39.3	60	1	US-08-256-964A-7	Sequence 7, Appl	C 793	11.2	38.6	31	1	US-08-323-531-71	Sequence 71, Appl
C 721	11.4	39.3	60	3	US-08-911-894-64	Sequence 64, Appl	C 794	11.2	38.6	31	1	US-08-435-634-236	Sequence 236, App
C 722	11.4	39.3	63	4	US-09-402-532-41	Sequence 41, Appl	C 795	11.2	38.6	31	1	US-08-435-634-237	Sequence 237, App
C 723	11.4	39.3	63	4	US-09-680-420A-23	Sequence 23, Appl	C 796	11.2	38.6	31	1	US-08-198-094-71	Sequence 71, Appl
C 724	11.4	39.3	63	4	US-09-621-976-18733	Sequence 18733, A	C 797	11.2	38.6	31	3	US-08-480-640A-119	Sequence 119, App
C 725	11.4	39.3	64	1	US-08-144-212-7	Sequence 7, Appl	C 798	11.2	38.6	31	3	US-08-295-802-119	Sequence 119, App
C 726	11.4	39.3	64	1	US-08-144-212-14	Sequence 14, Appl	C 799	11.2	38.6	31	3	US-08-107-794A-71	Sequence 71, Appl
C 727	11.4	39.3	67	1	US-08-306-285-2	Sequence 2, Appl	C 800	11.2	38.6	31	3	US-08-488-237A-119	Sequence 119, App
C 728	11.4	39.3	69	3	US-07-927-391-10	Sequence 10, Appl	C 801	11.2	38.6	31	4	US-08-375-992A-119	Sequence 119, App
C 729	11.4	39.3	70	1	US-08-217-210B-8	Sequence 8, Appl	C 802	11.2	38.6	31	4	US-09-206-898-22	Sequence 22, Appl
C 730	11.4	39.3	70	3	US-09-364-380-29	Sequence 29, Appl	C 803	11.2	38.6	31	4	US-09-495-052-47	Sequence 47, Appl
C 731	11.4	39.3	70	4	US-09-621-976-13621	Sequence 12621, A	C 804	11.2	38.6	31	4	US-08-472-678H-119	Sequence 119, App
C 732	11.4	39.3	71	4	US-08-956-171E-2239	Sequence 2239, Ap	C 805	11.2	38.6	31	4	US-09-247-890-4	Sequence 4, Appl
C 733	11.4	39.3	71	4	US-08-956-171E-1716	Sequence 1716, Ap	C 806	11.2	38.6	31	4	US-09-724-969-4	Sequence 4, Appl
C 734	11.4	39.3	79	3	US-08-932-082-12	Sequence 12, Appl	C 807	11.2	38.6	31	4	US-10-112-802-10	Sequence 10, Appl
C 735	11.4	39.3	79	4	US-09-861-687-12	Sequence 12, Appl	C 808	11.2	38.6	31	4	US-10-112-802-12	Sequence 12, Appl
C 736	11.4	39.3	80	1	US-08-472-255A-133	Sequence 133, App	C 809	11.2	38.6	31	5	PCT-US93-07424-71	Sequence 71, Appl
C 737	11.4	39.3	80	1	US-08-479-724A-133	Sequence 133, App	C 810	11.2	38.6	31	5	PCT-US95-02087-71	Sequence 71, Appl
C 738	11.4	39.3	80	3	US-08-472-256B-133	Sequence 133, App	C 811	11.2	38.6	31	5	PCT-US95-02087-71	Sequence 15, Appl
C 739	11.4	39.3	80	3	US-08-952-793-133	Sequence 133, App	C 812	11.2	38.6	33	1	US-08-201-118-25	Sequence 21, Appl
C 740	11.4	39.3	80	4	US-09-849-928-133	Sequence 133, App	C 813	11.2	38.6	33	1	US-08-201-118-25	Sequence 21, Appl
C 741	11.4	39.3	80	5	PCT-US96-09455A-133	Sequence 133, App	C 814	11.2	38.6	33	2	US-08-238-821B-15	Sequence 15, Appl
C 742	11.2	38.6	17	1	US-08-373-124A-1793	Sequence 1793, Ap	C 815	11.2	38.6	33	2	US-08-238-821B-21	Sequence 21, Appl
C 743	11.2	38.6	17	1	US-08-435-628-1793	Sequence 1793, Ap	C 816	11.2	38.6	33	3	US-09-121-425-10	Sequence 10, Appl
C 744	11.2	38.6	17	1	US-08-435-628-1793	Sequence 1793, Ap	C 817	11.2	38.6	33	3	US-09-344-700-28	Sequence 28, Appl
C 745	11.2	38.6	17	1	US-08-435-628-1793	Sequence 1793, Ap	C 818	11.2	38.6	33	4	US-09-265-653-7	Sequence 7, Appl
C 746	11.2	38.6	17	4	US-09-371-772B-5131	Sequence 5131, Ap	C 819	11.2	38.6	33	4	US-09-634-493A-10	Sequence 10, Appl
C 747	11.2	38.6	17	4	US-09-371-772B-5132	Sequence 5132, Ap	C 820	11.2	38.6	33	4	US-09-684-855-99	Sequence 99, Appl
C 748	11.2	38.6	17	4	US-09-827-998-280	Sequence 280, App	C 821	11.2	38.6	33	4	US-09-563-997A-28	Sequence 28, Appl
C 749	11.2	38.6	20	2	US-08-258-371-18	Sequence 18, Appl	C 822	11.2	38.6	33	5	PCT-US95-05744-15	Sequence 15, Appl
C 750	11.2	38.6	20	3	US-08-751-230-18	Sequence 18, Appl	C 823	11.2	38.6	33	5	PCT-US95-05744-21	Sequence 21, Appl
C 751	11.2	38.6	20	3	US-09-428-584-84	Sequence 84, Appl	C 824	11.2	38.6	34	3	US-08-408-774A-2	Sequence 2, Appl
C 752	11.2	38.6	20	3	US-09-428-584-85	Sequence 85, Appl	C 825	11.2	38.6	34	3	US-08-793-666-5	Sequence 5, Appl
C 753	11.2	38.6	20	3	US-09-428-584-86	Sequence 86, Appl	C 826	11.2	38.6	34	3	US-09-325-028-81	Sequence 81, Appl
C 754	11.2	38.6	20	3	US-09-428-584-86	Sequence 86, Appl	C 827	11.2	38.6	34	3	US-09-693-542-81	Sequence 81, Appl
C 755	11.2	38.6	20	3	US-09-499-082-18	Sequence 18, Appl	C 828	11.2	38.6	34	5	PCT-US96-03792-2	Sequence 2, Appl
C 756	11.2	38.6	20	3	US-09-313-932-340	Sequence 340, App	C 829	11.2	38.6	35	1	US-07-744-282C-105	Sequence 105, App
C 757	11.2	38.6	20	4	US-09-258-372-18	Sequence 18, Appl	C 830	11.2	38.6	35	1	US-08-497-312-8	Sequence 8, Appl

831	11.2	38.6	35	4	US-09-342-299-8	Sequence 8, Appli	11.2	38.6	38	4	US-09-371-772B-8225	Sequence 8225, Ap
832	11.2	38.6	35	5	PCT-US92-06821A-51	Sequence 51, Appl	11.2	38.6	38	4	US-09-371-772B-8448	Sequence 8448, Ap
833	11.2	38.6	36	1	US-08-291-932A-488	Sequence 488, App	11.2	38.6	38	4	US-09-371-772B-9921	Sequence 9921, Ap
834	11.2	38.6	36	1	US-08-334-847-163	Sequence 163, App	11.2	38.6	38	4	US-09-371-772B-10078	Sequence 10078, A
835	11.2	38.6	36	1	US-08-334-847-228	Sequence 228, App	11.2	38.6	38	4	US-09-371-772B-10731	Sequence 10731, A
836	11.2	38.6	36	1	US-08-334-847-375	Sequence 375, App	11.2	38.6	38	4	US-09-371-772B-10736	Sequence 10736, A
837	11.2	38.6	36	1	US-08-334-847-391	Sequence 391, App	11.2	38.6	38	4	US-09-371-772B-10907	Sequence 10907, A
838	11.2	38.6	36	1	US-08-334-847-745	Sequence 745, App	11.2	38.6	39	3	US-08-968-563-47	Sequence 47, Appl
839	11.2	38.6	36	1	US-08-334-847-772	Sequence 772, App	11.2	38.6	39	3	US-08-969-883A-47	Sequence 47, Appl
840	11.2	38.6	36	1	US-08-334-847-812	Sequence 812, App	11.2	38.6	39	4	US-08-297-928B-19	Sequence 19, Appl
841	11.2	38.6	36	1	US-08-334-847-821	Sequence 821, App	11.2	38.6	39	4	US-09-641-652-25	Sequence 25, Appl
842	11.2	38.6	36	1	US-08-334-847-832	Sequence 832, App	11.2	38.6	39	4	US-09-548-797B-137	Sequence 137, App
843	11.2	38.6	36	1	US-08-363-240A-286	Sequence 286, App	11.2	38.6	39	4	US-09-548-797B-138	Sequence 138, App
844	11.2	38.6	36	1	US-08-497-312-10	Sequence 10, Appl	11.2	38.6	40	4	US-09-605-192-9	Sequence 9, Appli
845	11.2	38.6	36	1	US-08-311-486C-394	Sequence 394, App	11.2	38.6	41	4	US-09-060-299-168	Sequence 168, App
846	11.2	38.6	36	1	US-08-311-486C-502	Sequence 502, App	11.2	38.6	41	4	US-08-402-923A-168	Sequence 168, App
847	11.2	38.6	36	1	US-08-311-486C-979	Sequence 979, App	11.2	38.6	42	3	US-08-491-954-34	Sequence 34, Appl
848	11.2	38.6	36	1	US-08-311-486C-979	Sequence 979, App	11.2	38.6	43	2	US-08-343-443B-38	Sequence 38, Appl
849	11.2	38.6	36	2	US-08-292-620A-888	Sequence 888, App	11.2	38.6	43	3	US-09-042-353-398	Sequence 398, App
850	11.2	38.6	36	2	US-08-585-684B-486	Sequence 486, App	11.2	38.6	43	4	US-08-758-417A-248	Sequence 248, App
851	11.2	38.6	36	2	US-08-585-684B-489	Sequence 489, App	11.2	38.6	43	4	US-08-171-389-29	Sequence 29, Appl
852	11.2	38.6	36	2	US-08-585-684B-1820	Sequence 1820, Ap	11.2	38.6	45	1	US-08-123-936-29	Sequence 29, Appl
853	11.2	38.6	36	2	US-08-585-684B-2010	Sequence 2010, Ap	11.2	38.6	45	1	US-08-852-449A-5	Sequence 5, Appli
854	11.2	38.6	36	3	US-08-585-684B-2028	Sequence 2028, Ap	11.2	38.6	45	2	US-08-475-228A-29	Sequence 29, Appl
855	11.2	38.6	36	3	US-08-491-954-52	Sequence 52, Appl	11.2	38.6	45	3	US-08-482-080A-29	Sequence 29, Appl
856	11.2	38.6	36	3	US-09-071-845-888	Sequence 888, App	11.2	38.6	45	4	US-09-354-947-29	Sequence 29, Appl
857	11.2	38.6	36	3	US-08-862-540-17	Sequence 17, Appl	11.2	38.6	45	5	PCT-US93-12388-29	Sequence 29, Appl
858	11.2	38.6	36	3	US-09-038-073-486	Sequence 486, App	11.2	38.6	47	3	US-09-338-907-203	Sequence 203, App
859	11.2	38.6	36	3	US-09-038-073-489	Sequence 489, App	11.2	38.6	47	4	US-09-218-207-203	Sequence 203, App
860	11.2	38.6	36	3	US-09-038-073-1620	Sequence 1620, Ap	11.2	38.6	47	4	US-08-641-638-748	Sequence 748, App
861	11.2	38.6	36	3	US-09-038-073-2010	Sequence 2010, Ap	11.2	38.6	47	4	US-08-641-638-1230	Sequence 1230, Ap
862	11.2	38.6	36	3	US-09-038-073-2028	Sequence 2028, Ap	11.2	38.6	47	4	US-09-422-978-702	Sequence 702, App
863	11.2	38.6	36	4	US-09-633-043-17	Sequence 17, Appl	11.2	38.6	47	4	US-09-422-978-844	Sequence 844, App
864	11.2	38.6	37	2	US-08-343-923-8	Sequence 8, Appli	11.2	38.6	47	4	US-09-422-978-974	Sequence 974, App
865	11.2	38.6	38	1	US-08-373-124A-707	Sequence 707, App	11.2	38.6	47	4	US-09-422-978-1433	Sequence 1433, App
866	11.2	38.6	38	1	US-08-373-124A-745	Sequence 745, App	11.2	38.6	47	4	US-09-422-978-1538	Sequence 1538, Ap
867	11.2	38.6	38	1	US-08-373-124A-949	Sequence 949, App	11.2	38.6	47	4	US-09-422-978-1662	Sequence 1662, Ap
868	11.2	38.6	38	1	US-08-373-124A-969	Sequence 969, App	11.2	38.6	47	4	US-08-422-978-1676	Sequence 1676, Ap
869	11.2	38.6	38	1	US-08-373-124A-1147	Sequence 1147, Ap	11.2	38.6	47	4	US-09-422-978-2402	Sequence 2402, Ap
870	11.2	38.6	38	1	US-08-373-124A-1806	Sequence 1806, Ap	11.2	38.6	47	4	US-09-422-978-2405	Sequence 2405, Ap
871	11.2	38.6	38	1	US-08-373-124A-1814	Sequence 1814, Ap	11.2	38.6	47	4	US-09-422-978-2903	Sequence 2903, Ap
872	11.2	38.6	38	1	US-08-373-124A-1814	Sequence 1814, Ap	11.2	38.6	47	4	US-09-422-978-3087	Sequence 3087, Ap
873	11.2	38.6	38	1	US-08-373-124A-1886	Sequence 1886, Ap	11.2	38.6	47	4	US-09-422-978-3596	Sequence 3596, Ap
874	11.2	38.6	38	1	US-08-435-628-707	Sequence 707, App	11.2	38.6	47	4	US-09-422-978-3604	Sequence 3604, Ap
875	11.2	38.6	38	1	US-08-435-628-745	Sequence 745, App	11.2	38.6	47	4	US-09-422-978-3823	Sequence 3823, Ap
876	11.2	38.6	38	1	US-08-435-628-949	Sequence 949, App	11.2	38.6	48	1	US-08-471-791-36	Sequence 36, Appl
877	11.2	38.6	38	1	US-08-435-628-969	Sequence 969, App	11.2	38.6	48	2	US-08-477-553A-17	Sequence 17, Appl
878	11.2	38.6	38	1	US-08-435-628-1147	Sequence 1147, Ap	11.2	38.6	48	4	US-09-586-546-43	Sequence 43, Appl
879	11.2	38.6	38	1	US-08-435-628-1806	Sequence 1806, Ap	11.2	38.6	48	4	US-09-065-914B-2	Sequence 2, Appli
880	11.2	38.6	38	1	US-08-435-628-1806	Sequence 1806, Ap	11.2	38.6	48	5	PCT-US91-01746-36	Sequence 36, Appl
881	11.2	38.6	38	1	US-08-435-628-1834	Sequence 1834, Ap	11.2	38.6	50	1	US-08-171-389-442	Sequence 442, App
882	11.2	38.6	38	1	US-08-435-628-1886	Sequence 1886, Ap	11.2	38.6	50	1	US-08-123-936-442	Sequence 442, App
883	11.2	38.6	38	2	US-08-292-620A-2133	Sequence 2133, Ap	11.2	38.6	50	2	US-08-475-228A-442	Sequence 442, App
884	11.2	38.6	38	3	US-09-071-845-2133	Sequence 2133, Ap	11.2	38.6	50	3	US-08-482-080A-442	Sequence 442, App
885	11.2	38.6	38	3	US-09-454-704A-7	Sequence 7, Appli	11.2	38.6	50	4	US-08-849-567A-70	Sequence 70, Appl
886	11.2	38.6	38	4	US-09-371-772B-7628	Sequence 7628, Ap	11.2	38.6	50	4	US-08-849-567A-78	Sequence 78, Appl
887	11.2	38.6	38	4	US-09-371-772B-7873	Sequence 7873, Ap	11.2	38.6	50	4	US-09-947-442	Sequence 442, App
888	11.2	38.6	38	4	US-09-371-772B-7876	Sequence 7876, Ap	11.2	38.6	50	4	US-09-354-929-35	Sequence 35, Appl
889	11.2	38.6	38	4	US-09-371-772B-7878	Sequence 7878, Ap	11.2	38.6	50	4	US-09-554-929-160	Sequence 160, App
890	11.2	38.6	38	4	US-09-371-772B-7878	Sequence 7878, Ap	11.2	38.6	50	4	US-09-443-199C-499	Sequence 499, App
891	11.2	38.6	38	4	US-09-371-772B-7992	Sequence 7992, Ap	11.2	38.6	50	4	US-09-443-199C-843	Sequence 843, App
892	11.2	38.6	38	4	US-09-371-772B-8014	Sequence 8014, Ap	11.2	38.6	50	5	PCT-US93-12388-442	Sequence 442, App
893	11.2	38.6	38	4	US-09-371-772B-8044	Sequence 8044, Ap	11.2	38.6	51	4	US-09-443-199C-511	Sequence 511, App
894	11.2	38.6	38	4	US-09-371-772B-8138	Sequence 8138, Ap	11.2	38.6	51	4	US-09-443-199C-844	Sequence 844, App
895	11.2	38.6	38	4	US-09-371-772B-8214	Sequence 8214, Ap	11.2	38.6	51	4	US-08-585-684B-2524	Sequence 2524, Ap
896	11.2	38.6	38	4	US-09-371-772B-8217	Sequence 8217, Ap	11.2	38.6	54	3	US-08-038-073-2524	Sequence 2524, Ap
897	11.2	38.6	38	4	US-09-371-772B-8218	Sequence 8218, Ap	11.2	38.6	54	3	US-08-956-171E-3400	Sequence 3400, Ap
898	11.2	38.6	38	4	US-09-371-772B-8219	Sequence 8219, Ap	11.2	38.6	55	1	US-08-395-381C-3	Sequence 3, Appli
899	11.2	38.6	38	4	US-09-371-772B-8220	Sequence 8220, Ap	11.2	38.6	55	2	US-08-701-124-12	Sequence 12, Appl
900	11.2	38.6	38	4	US-09-371-772B-8221	Sequence 8221, Ap	11.2	38.6	55	2	US-08-700-846-12	Sequence 12, Appl
901	11.2	38.6	38	4	US-09-371-772B-8222	Sequence 8222, Ap	11.2	38.6	55	2	US-08-563-368B-9	Sequence 9, Appli
902	11.2	38.6	38	4	US-09-371-772B-8223	Sequence 8223, Ap	11.2	38.6	55	3	US-09-130-225-12	Sequence 12, Appl
903	11.2	38.6	38	4	US-09-371-772B-8224	Sequence 8224, Ap	11.2	38.6	55	4	US-09-455-061-12	Sequence 12, Appl

c 977 11.2 38.6 55 4 US-09-101-751A-9
c 978 11.2 38.6 55 4 US-09-326-447-3
c 979 11.2 38.6 55 4 US-08-956-171E-2196
c 980 11.2 38.6 55 4 US-09-969-192-12
c 981 11.2 38.6 57 1 US-08-395-381C-4
c 982 11.2 38.6 57 2 US-08-701-124-13
c 983 11.2 38.6 57 2 US-08-700-846-13
c 984 11.2 38.6 57 2 US-08-563-368B-10
c 985 11.2 38.6 57 2 US-09-130-225-13
c 986 11.2 38.6 57 4 US-09-455-061-13
c 987 11.2 38.6 57 4 US-09-101-751A-10
c 988 11.2 38.6 57 4 US-09-326-447-4
c 989 11.2 38.6 57 4 US-09-969-192-13
c 990 11.2 38.6 59 1 US-08-117-374-7
c 991 11.2 38.6 59 1 US-08-280-263-7
c 992 11.2 38.6 59 3 US-08-597-325-7
c 993 11.2 38.6 59 3 US-08-597-325-7
c 994 11.2 38.6 59 5 PCT-US94-10256-7
c 995 11.2 38.6 60 3 US-08-896-449A-3
c 996 11.2 38.6 60 3 US-09-132-652-3
c 997 11.2 38.6 60 3 US-09-046-247-47
c 998 11.2 38.6 60 4 US-09-626-929-22
c 999 11.2 38.6 60 4 US-09-484-850-22
c1000 11.2 38.6 60 4 US-09-408-392-22

ALIGNMENTS

RESULT 1
US-08-667-079B-5/C
; Sequence 5, Application US/08667079B
; Patent No. 5789171
; GENERAL INFORMATION:
; APPLICANT: Mark S. Smeltzer
; TITLE OF INVENTION: Use of cna, fnbA, fnbB, and hlb Gene Probes for the Strain-Sp
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, MCGREGOR & ADLER, P.C.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,079B
; FILING DATE: June 20, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Benjamin Aaron
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: No
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINES:
US-08-667-079B-5
Query Match 52.4%; Score 15.2; DB 1; Length 33;
Best Local Similarity 42.9%; Pred. No. 4e+02;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
Qy 2 AGAUCUUUUUGUAGCCCAAGGCGCU 29
Db 32 ATGATGTTTATTAGTTCCTCCCGGCT 5
RESULT 2
US-09-422-978-1097
; Sequence 1097, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET-020CE1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1097
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2043-220 : polymorphic base A or T
US-09-422-978-1097
Query Match 52.4%; Score 15.2; DB 4; Length 47;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
Qy 3 AGAUCUUUUUGUAGCCCAAA 24
Db 15 AGACTCTTTWTGTACCTCCCA 36
RESULT 3
US-07-971-101-6/C
; Sequence 6, Application US/07971101
; Patent No. 5443969
; GENERAL INFORMATION:
; APPLICANT: Wilson, Thomas M.A. et al.
; TITLE OF INVENTION: RNA Packaging System
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25


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; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,950
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/515,236
; FILING DATE: 15-AUG-1995
; APPLICATION NUMBER: US 08/219,633
; FILING DATE: 28-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-5353
; TELEFAX: (608) 257-9175
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-761-950-25

Query Match 51.0%; Score 14.8; DB 1; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGUAGCCCAAGGCU 29
Db 29 GATTATCTTATCATCCACTAGGCT 4

RESULT 7
US-08-632-575B-39/c
; Sequence 39, Application US/08632575B
; Patent No. 5843660
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; TITLE OF INVENTION: Multiplex Amplification of
; TITLE OF INVENTION: Short tandem Repeat Loci
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: DOS, version 6.0
; SOFTWARE: WordPerfect 5.1 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,575B
; FILING DATE: 04/15/96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/316,544
; FILING DATE: 09/30/94
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29

; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/327,229
; FILING DATE: 07-Jun-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,544
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-327-229-31

Query Match 51.0%; Score 14.8; DB 3; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGUAGCCCAAGGCU 29
Db 29 GATTATCTTATCATCCACTAGGCT 4

RESULT 9
US-09-199-542B-39/c
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; Sequence 39, Application US/09199542B
; Patent No. 6479235
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; TITLE OF INVENTION: Multiplex Amplification of Short Tandem Repeat Loci
; FILE REFERENCE: 16026/9212
; CURRENT APPLICATION NUMBER: US/09/199,542B
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 08/316,544
; PRIOR FILING DATE: 1994-09-30
; PRIOR APPLICATION NUMBER: US 08/632,575
; PRIOR FILING DATE: 1996-04-15
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Word97 (converted to DOS text format)
; SEQ ID NO 39
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapien
; LOCATION: HUMWPA31
US-09-199-542B-39

Query Match 51.0%; Score 14.8; DB 4; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02; 7; Indels 0; Gaps 0;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGAAGCCCAAGGCGU 29
DB 29 GATTATCTTATCATCCACTAGGGCT 4

RESULT 10
PCT-US95-12608-31/c
; Sequence 31, Application PC/TUS9512608
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; APPLICANT: Lins, Ann M.
; TITLE OF INVENTION: MULTIPLEX AMPLIFICATION OF SHORT TANDEM
; TITLE OF INVENTION: REPEAT LOCI
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: P. O. Box 2599
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12608
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-12608-31

Query Match 51.0%; Score 14.8; DB 5; Length 29;
Best Local Similarity 42.3%; Pred. No. 6e+02; 7; Indels 0; Gaps 0;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGAAGCCCAAGGCGU 29
DB 29 GATTATCTTATCATCCACTAGGGCT 4

RESULT 11
US-08-632-575B-59/c
; Sequence 59, Application US/08632575B
; Patent No. 5843660
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; TITLE OF INVENTION: Multiplex Amplification of
; TITLE OF INVENTION: Short Tandem Repeat Loci
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: DOS, version 6.0
; SOFTWARE: WordPerfect 5.1 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,575B
; FILING DATE: 04/15/96
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/316,544
; FILING DATE: 09/30/94
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; POSITION IN GENOME:
; MAP POSITION: HUMWPA31
US-08-632-575B-59

Query Match 51.0%; Score 14.8; DB 2; Length 32;
Best Local Similarity 42.3%; Pred. No. 6.1e+02; 7; Indels 0; Gaps 0;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGAAGCCCAAGGCGU 29
DB 29 GATTATCTTATCATCCACTAGGGCT 4

RESULT 12
US-09-199-542B-59/c
; Sequence 59, Application US/09199542B
; Patent No. 6479235
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; TITLE OF INVENTION: Multiplex Amplification of Short Tandem Repeat Loci
; FILE REFERENCE: 16026/9212
; CURRENT APPLICATION NUMBER: US/09/199,542B
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 08/316,544
; PRIOR FILING DATE: 1994-09-30
; PRIOR APPLICATION NUMBER: US 08/632,575
; PRIOR FILING DATE: 1996-04-15
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Word97 (converted to DOS text format)

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; SEQ ID NO 59
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Homo sapien
; LOCATION: HUMVFA31
US-09-199-542B-59

Query Match
  51.0%; Score 14.8; DB 4; Length 32;
Best Local Similarity 42.3%; Pred. No. 6.1e+02;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGUAGCCCAAGGCT 29
|||: : : : : |||:
29 GATTATCTTATCATCCACTAGGCT 4

Db

RESULT 13
US-09-063-733A-18
; Sequence 18, Application US/09063733A
; Patent No. 6372211
; GENERAL INFORMATION:
; APPLICANT: Isaac, Barbara G.
; APPLICANT: Greenplate, John T.
; APPLICANT: Purcell, John P.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,733A
; FILING DATE: 21-APR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOST:022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-787-1440
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-063-733A-18

Query Match
  50.3%; Score 14.6; DB 4; Length 25;
Best Local Similarity 47.6%; Pred. No. 7.2e+02;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAGUUCUUUUUGUAGCCCAAGGCT 22
|||: : : : : |||:
5 AAGCTTCTCTTGTATATACC 25

Db

RESULT 14
US-08-486-969-46/c
; Sequence 46, Application US/08486969
; Patent No. 5843456
; GENERAL INFORMATION:
```

```
; APPLICANT: Paoletti, Enzo
; APPLICANT: Maki, Joanne
; TITLE OF INVENTION: RECOMBINANT POXVIRUS - RABIES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,969
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-486-969-46

Query Match
  50.3%; Score 14.6; DB 2; Length 53;
Best Local Similarity 47.8%; Pred. No. 8.3e+02;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 9 UUUUUGUAGCCCAAGGCT 29
||||: |||: |||:
Db 29 TTTTGTAGCTTCCCGGCT 9

RESULT 15
US-09-827-998-1098/c
; Sequence 1098, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 1098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1098

Query Match
  49.0%; Score 14.2; DB 4; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
```


FILE REFERENCE: MDNMORF-8
CURRENT APPLICATION NUMBER: US/09/827,998
EARLIER FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6656700
SEQ ID NO 1103
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-827-998-1103

Query Match 49.0%; Score 14.2; DB 4; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAGCCCCAAG 25
:|||||:|||||
Db 20 TCTTTTGTAGTCCCTAAG 2

RESULT 21
US-09-827-998-1104/c
Sequence 1104; Application US/09827998
Patent No. 6656700
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MDNMORF-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6656700
SEQ ID NO 1104
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-827-998-1104

Query Match 49.0%; Score 14.2; DB 4; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+03;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAGCCCCAAG 25
:|||||:|||||
Db 19 TCTTTTGTAGTCCCTAAG 1

RESULT 22
US-09-422-978-96
Sequence 96; Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 96
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-12847-37 : polymorphic base A or G
US-09-422-978-96

Query Match 49.0%; Score 14.2; DB 4; Length 47;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 9; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 9 UUUUUUAGCCCCAAGGCGU 29
:|||||:|||||
Db 8 TTTTCTAAGTCCACRGCT 28

RESULT 23
US-08-410-654B-30
Sequence 30; Application US/08410654B
Patent No. 5833976
GENERAL INFORMATION:
APPLICANT: Rene de Waal Malefyt
APPLICANT: Di-Hwei Hsu
APPLICANT: Anne O'Garra
APPLICANT: Hergen Spits
TITLE OF INVENTION: Use of Interleukin-10 to Treat
TITLE OF INVENTION: Septic Shock
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,654B
FILING DATE: 24-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQ1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-410-654B-30

Query Match 49.0%; Score 14.2; DB 2; Length 69;
Best Local Similarity 51.9%; Pred. No. 1.3e+03;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AAAGAUUUUUUUUAAGCCCAAGG 27
Db 7 AAGAATGCCTTTAATAAGTCCAAGAG 33

RESULT 24

US-08-474-851-30
; Sequence 30, Application US/08474851
; Patent No. 5837232
; GENERAL INFORMATION:
; APPLICANT: Rene de Waal Malefyt
; APPLICANT: Di-Hwei Hsu
; APPLICANT: Anne O'Garra
; APPLICANT: Hergen Spits
; TITLE OF INVENTION: Use of An Interleukin-10 Antagonist to Treat
; TITLE OF INVENTION: A B Cell Mediated Autoimmune Disorder
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,851
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,654
FILING DATE: 24-MAR-1995
APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQ1GD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)

US-08-474-851-30

Query Match 49.0%; Score 14.2; DB 2; Length 69;
Best Local Similarity 51.9%; Pred. No. 1.3e+03;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AAAGAUUUUUUUUAAGCCCAAGG 27
Db 7 AAGAATGCCTTTAATAAGTCCAAGAG 33

RESULT 25

US-08-481-560-30
; Sequence 30, Application US/08481560
; Patent No. 5837293
; GENERAL INFORMATION:
; APPLICANT: Rene de Waal Malefyt
; APPLICANT: Di-Hwei Hsu
; APPLICANT: Anne O'Garra
; APPLICANT: Hergen Spits
; TITLE OF INVENTION: Use of Interleukin-10 to Modulate
; TITLE OF INVENTION: Inflammation or T-Cell Mediated
; TITLE OF INVENTION: Immune Function
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,560
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,654
FILING DATE: 24-MAR-1995
APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQ1GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)

US-08-481-560-30

Query Match 49.0%; Score 14.2; DB 2; Length 69;
Best Local Similarity 51.9%; Pred. No. 1.3e+03;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AAAGAUUUUUUUUAAGCCCAAGG 27
Db 7 AAGAATGCCTTTAATAAGTCCAAGAG 33

RESULT 26

US-09-571-774-2
; Sequence 2, Application US/09571774
; Patent No. 6479262
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; TITLE OF INVENTION: Solid Phase Enzymatic Assembly of Polynucleotides
; FILE REFERENCE: HER-0005
; CURRENT APPLICATION NUMBER: US/09/571,774
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 4

;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 41
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Primer Oligonucleotide
US-09-571-774-2

Query Match 48.3%; Score 14; DB 4; Length 41;
Best Local Similarity 54.5%; Pred. No. 1.5e+03;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGAUCUUUUUGUAGCCCA 24
|||:|:|:|:|:|:|:|:|:|
Db 15 AGATTCCTCGTAGCCCAA 36

RESULT 27

US-09-852-385-2
; Sequence 2, Application US/09852385
; Patent No. 6635453
; GENERAL INFORMATION:
; APPLICANT: Delgrave, Simon
; APPLICANT: Marrs, Barry
; TITLE OF INVENTION: Methods For The Enzymatic Assembly Of Polynucleotides And Identification Of Polynucleotides Having Desired Characteristics
; FILE REFERENCE: HER-0042
; CURRENT APPLICATION NUMBER: US/09/852,385
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/571,774
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6635453el Sequence
US-09-852-385-2

Query Match 48.3%; Score 14; DB 4; Length 41;
Best Local Similarity 54.5%; Pred. No. 1.5e+03;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGAUCUUUUUGUAGCCCA 24
|||:|:|:|:|:|:|:|:|:|
Db 15 AGATTCCTCGTAGCCCAA 36

RESULT 28

US-08-943-731-336/c
; Sequence 336, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISSA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: ALA-KORKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND

;; STREET: ELR.
;; CITY: PHILADELPHIA
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103-7086
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/943,731
;; FILING DATE: 03-OCT-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION NUMBER: US 08/212,322
;; FILING DATE: 14-MAR-1994
;; APPLICATION NUMBER: US 07/803,628
;; FILING DATE: 03-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DOYLE LEARY Ph.D., KATHRYN
;; REGISTRATION NUMBER: 36,317
;; REFERENCE/DOCKET NUMBER: 9598-27
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-965-1284
;; TELEFAX: 215-567-2991
;; TELEX: 831-494
;; INFORMATION FOR SEQ ID NO: 336:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-943-731-336

Query Match 47.6%; Score 13.8; DB 3; Length 25;
Best Local Similarity 47.1%; Pred. No. 1.7e+03;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AUUCUUUUUGUAGCCC 21
|||:|:|:|:|:|:|:|:|:|
Db 22 ATTCTTTGTGAGCCC 6

RESULT 29

US-09-199-542B-76/c
; Sequence 76, Application US/09199542B
; Patent No. 6479235
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; TITLE OF INVENTION: Multiplex Amplification of Short Tandem Repeat Loci
; FILE REFERENCE: 16026/9212
; CURRENT APPLICATION NUMBER: US/09/199,542B
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 08/316,544
; PRIOR FILING DATE: 1994-09-30
; PRIOR APPLICATION NUMBER: US 08/632,575
; PRIOR FILING DATE: 1996-04-15
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Word97 (converted to DOS text format)
; SEQ ID NO 76
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapien
; LOCATION: HUMWFA31
US-09-199-542B-76

Query Match 47.6%; Score 13.8; DB 4; Length 33;
Best Local Similarity 44.0%; Pred. No. 1.8e+03;
Matches 11; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

```
QY 4 GAUUCUUUUUUAAGCCCCCAAGGCG 28
Db 25 GATTATCTTATCATCCACTAGGCG 1

RESULT 30
US-09-671-317-663/c
; Sequence 663, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 663
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 12-345-453 : polymorphic base G or C
US-09-671-317-663

Query Match 47.6%; Score 13.8; DB 4; Length 47;
Best Local Similarity 37.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGAUUCUUUUUUAAGCCCCCAAGGCG 28
Db 47 AGATTATTTTATACCCCAATAGGAC 21

RESULT 31
US-09-428-082B-401/c
; Sequence 401, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 401
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-FC
US-09-428-082B-401

Query Match 47.6%; Score 13.8; DB 4; Length 47;
Best Local Similarity 37.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 2 AGAUUCUUUUUUAAGCCCCCAAGGCG 28
Db 47 AGATTATTTTATACCCCAATAGGAC 21

RESULT 31
US-09-428-082B-401/c
; Sequence 401, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 401
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-FC
US-09-428-082B-401

Query Match 47.6%; Score 13.8; DB 4; Length 47;
Best Local Similarity 37.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
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```
QY 11 UUUGUAGCCCCCAAGG 27
Db 49 TATGTAAGCCCAAGG 33

RESULT 32
US-09-428-082B-414
; Sequence 414, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 414
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-EMP-FC
US-09-428-082B-414

Query Match 47.6%; Score 13.8; DB 4; Length 57;
Best Local Similarity 70.6%; Pred. No. 2e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 UUUGUAGCCCCCAAGG 27
Db 2 TATGTAAGCCCAAGG 18

RESULT 33
US-09-428-082B-415/c
; Sequence 415, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 415
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-EMP-FC
US-09-428-082B-415

Query Match 47.6%; Score 13.8; DB 4; Length 60;
Best Local Similarity 70.6%; Pred. No. 2e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 UUUGUAGCCCCCAAGG 27
```


Db 37 AAAGCTAATCTTGAAGGCTCCATGGC 10

RESULT 38
US-09-310-463-6
; Sequence 6, Application US/09310463A
; Patent No. 6384203
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
; TITLE OF INVENTION: Like Receptors (LIR)
; FILE REFERENCE: 2624-A
; CURRENT APPLICATION NUMBER: US/09/310,463A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 08/842,248
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 52
; TYPE: DNA
; ORGANISM: human
; US-09-310-463-6

Query Match 46.9%; Score 13.6; DB 4; Length 52;
Best Local Similarity 46.4%; Pred. No. 2.4e+03;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUUAAGCCCCCAAGGCG 28
Db 22 AGATCTTCTCTATACCCCAAGGTGC 49

RESULT 39
US-08-842-248A-6
; Sequence 6, Application US/08842248A
; Patent No. 6448035
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Family of Immunoregulators Designated
; TITLE OF INVENTION: Leukocyte Immunoglobulin-Like Receptors (LIR)
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM/PC Compatible
; OPERATING SYSTEM: Microsoft Word 7.0
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/842,248A
; FILING DATE: April 24, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C.
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single

Db 37 AAAGCTAATCTTGAAGGCTCCATGGC 10

US-08-842-248A-6

Query Match 46.9%; Score 13.6; DB 4; Length 52;
Best Local Similarity 46.4%; Pred. No. 2.4e+03;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUUAAGCCCCCAAGGCG 28
Db 22 AGATCTTCTCTATACCCCAAGGTGC 49

RESULT 40
US-08-472-255A-136/C
; Sequence 136, Application US/08472255A
; Patent No. 5766853
; GENERAL INFORMATION:
; APPLICANT: PARMA, DAVID
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
; TITLE OF INVENTION: TO SELECTINS (AS AMENDED)
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,255A
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX40-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-472-255A-136

Query Match 46.9%; Score 13.6; DB 1; Length 79;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 AAAGAUUUUUUUUAAGCCCCCAAGGCG 29
Db 49 AGAGCTTCTCTATGAGGCCCAAGGGT 22

us-09-310-844c-25.max.rni

Tue Apr 20 10:03:05 2004

Search completed: April 18, 2004, 10:00:00
Job time : 42.6667 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 07:30:54 ; Search time 1527.67 Seconds

(without alignments)
566.880 Million cell updates/sec

Title: US-09-310-844C-25

Perfect score: 29

Sequence: 1 aagaacuuuuuuuaagcccaagggu 29

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 375216

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_hcc.*

9: gb_est1.*

10: gb_est2.*

11: gb_est3.*

12: gb_est4.*

13: gb_est5.*

14: gb_est6.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18.4	63.4	70	9	AA516989
C 2	17.4	60.0	67	9	AA708911
C 3	16.6	57.2	70	9	AI609194
C 4	16.6	57.2	75	14	H07686

C 5	16	55.2	51	12	BG361927
C 6	16	55.2	73	12	BG361978
C 7	15.8	54.5	58	9	AI824019
C 8	15.8	54.5	72	13	BG613481
C 9	15.8	54.5	76	28	AZ657549
C 10	15.6	53.8	37	9	AI802260
C 11	15.6	53.8	58	28	AZ834846
C 12	15.4	53.1	47	14	U44334
C 13	15.4	53.1	77	28	BH252676
C 14	15.4	53.1	78	29	AG260396
C 15	15.2	52.4	61	9	AI318033
C 16	15.2	52.4	65	12	BM517546
C 17	15.2	52.4	78	9	AA936218
C 18	15.1	51.7	58	28	B02943
C 19	15.1	51.7	68	14	CD682098
C 20	14.8	51.0	34	28	AZ840876
C 21	14.8	51.0	49	28	AZ576537
C 22	14.8	51.0	55	9	AI224478
C 23	14.8	51.0	64	10	BE636255
C 24	14.8	51.0	67	29	CG588850
C 25	14.8	51.0	70	9	AL780467
C 26	14.8	51.0	76	28	B289798
C 27	14.8	51.0	77	29	CG549254
C 28	14.6	50.3	52	29	BX650715
C 29	14.6	50.3	53	29	AL940874
C 30	14.6	50.3	59	10	BE970792
C 31	14.6	50.3	61	13	BQ479345
C 32	14.6	50.3	65	29	AL763793
C 33	14.6	50.3	69	28	BZ768797
C 34	14.6	50.3	70	28	BZ768791
C 35	14.6	50.3	70	28	BZ768795
C 36	14.6	50.3	71	14	CE227161
C 37	14.6	50.3	71	28	AZ833202
C 38	14.6	50.3	75	9	AI696772
C 39	14.6	50.3	80	29	AL770832
C 40	14.6	50.3	80	29	BX662819
C 41	14.4	49.7	35	28	BH856246
C 42	14.4	49.7	35	28	BH856247
C 43	14.4	49.7	37	28	AZ950243
C 44	14.4	49.7	41	28	AZ598587
C 45	14.4	49.7	51	14	CF425249
C 46	14.4	49.7	51	29	DMES45740
C 47	14.4	49.7	56	28	BZ665747
C 48	14.4	49.7	57	12	BG362067
C 49	14.4	49.7	58	9	AV953887
C 50	14.4	49.7	64	9	AI321110
C 51	14.4	49.7	65	28	BH908271
C 52	14.4	49.7	66	12	BG361679
C 53	14.4	49.7	66	29	CG485985
C 54	14.4	49.7	67	28	BH848343
C 55	14.4	49.7	67	29	CG517699
C 56	14.4	49.7	67	29	CG474006
C 57	14.4	49.7	67	29	CG474744
C 58	14.4	49.7	67	29	CG475921
C 59	14.4	49.7	67	29	CG476132
C 60	14.4	49.7	67	29	CG476342
C 61	14.4	49.7	67	29	CG476342
C 62	14.4	49.7	67	29	CG476917
C 63	14.4	49.7	67	29	CG477123
C 64	14.4	49.7	67	29	CG477690
C 65	14.4	49.7	67	29	CG477783
C 66	14.4	49.7	67	29	CG479801
C 67	14.4	49.7	67	29	CG480240
C 68	14.4	49.7	67	29	CG480439
C 69	14.4	49.7	67	29	CG480503
C 70	14.4	49.7	67	29	CG480672
C 71	14.4	49.7	67	29	CG480879
C 72	14.4	49.7	67	29	CG480941
C 73	14.4	49.7	67	29	CG480982
C 74	14.4	49.7	67	29	CG481136
C 75	14.4	49.7	67	29	CG481158
C 76	14.4	49.7	67	29	CG481469
C 77	14.4	49.7	67	29	CG482313

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BG613481	id07h06.y
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AI802260	tj36g07.x
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U44334	ENU44334.AS
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AG260396	Lotus cor
AI318033	ta75g02.x
BM517546	KJ80907.y
AA936218	on43c10.s
B02943	CSRL-163G2-
CD682098	ij46c08.y
AZ840876	2M0138C08
AZ576537	AST-T11C0
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AL780467	AL780467
B289798	SALK 0232
CG549254	OST152329
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BQ479345	ku3d12.y
AL763793	Arabidops
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AZ598587	IM0413A04
CF425249	lad09g02
AJ545740	Drosophila
BZ665747	KG10262.D
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AV953887	AV953887
AI321110	d4c09nm.r
BH908271	SALK 0468
BG361679	gb48d04.y
CG485985	OST20677
BH848343	SALK 0578
CG517699	CH240_364
CG474006	OST1820.M
CG474744	OST2811.M
CG475921	OST4838.M
CG476132	OST5408.M
CG476342	OST5686.M
CG476342	OST5739.M
CG476917	OST6599.M
CG477123	OST6898.M
CG477690	OST7684.M
CG477783	OST7811.M
CG479801	OST11140
CG480240	OST12006
CG480439	OST12343
CG480503	OST12440
CG480672	OST12696
CG480879	OST13018
CG480941	OST13120
CG480982	OST13178
CG481136	OST13426
CG481158	OST13486
CG481469	OST13911
CG482313	OST15297

C 78	14.4	49.7	67	29	CG482838	OST16124	CG482838	OST16124	151	14.4	49.7	72	29	EX224205	Danio rer
C 79	14.4	49.7	67	29	CG482887	OST16195	CG482887	OST16195	152	14.4	49.7	73	12	BM568281	sal102402.
C 80	14.4	49.7	67	29	CG482965	OST16319	CG482965	OST16319	153	14.4	49.7	74	29	CG574740	GB207881
C 81	14.4	49.7	67	29	CG483071	OST16504	CG483071	OST16504	C 154	14.4	49.7	76	12	BG361288	GB66a08.Y
C 82	14.4	49.7	67	29	CG484155	OST18008	CG484155	OST18008	C 155	14.4	49.7	76	13	BQ393681	BQ393681
C 83	14.4	49.7	67	29	CG484480	OST18444	CG484480	OST18444	C 156	14.4	49.7	76	28	AQ025263	AQ025263
C 84	14.4	49.7	67	29	CG484698	OST18749	CG484698	OST18749	C 157	14.4	49.7	77	14	CS262321	CS262321
C 85	14.4	49.7	67	29	CG484811	OST18895	CG484811	OST18895	C 158	14.4	49.7	77	14	CS262321	CS262321
C 86	14.4	49.7	67	29	CG484964	OST19117	CG484964	OST19117	C 159	14.4	49.7	78	13	BQ244462	BQ244462
C 87	14.4	49.7	67	29	CG485056	OST19253	CG485056	OST19253	C 160	14.4	49.7	80	29	CG570907	CG570907
C 88	14.4	49.7	67	29	CG485118	OST19344	CG485118	OST19344	C 161	14.2	49.0	38	28	BZ355014	BZ355014
C 89	14.4	49.7	67	29	CG485130	OST19361	CG485130	OST19361	C 162	14.2	49.0	40	29	CG779591	CG779591
C 90	14.4	49.7	67	29	CG485219	OST19496	CG485219	OST19496	C 163	14.2	49.0	40	29	BQ5408	BQ5408
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C 92	14.4	49.7	67	29	CG486069	OST20815	CG486069	OST20815	C 165	14.2	49.0	59	14	CH258816	CH258816
C 93	14.4	49.7	67	29	CG486451	OST21486	CG486451	OST21486	C 166	14.2	49.0	62	29	CG559308	CG559308
C 94	14.4	49.7	67	29	CG486698	OST21859	CG486698	OST21859	C 167	14.2	49.0	64	29	BX161966	BX161966
C 95	14.4	49.7	67	29	CG486795	OST21978	CG486795	OST21978	C 168	14.2	49.0	65	9	AI1719509	AI1719509
C 96	14.4	49.7	67	29	CG486884	OST22098	CG486884	OST22098	C 169	14.2	49.0	65	13	BQ564818	BQ564818
C 97	14.4	49.7	67	29	CG486890	OST22107	CG486890	OST22107	C 170	14.2	49.0	69	9	AI211081	AI211081
C 98	14.4	49.7	67	29	CG486923	OST22154	CG486923	OST22154	C 171	14.2	49.0	71	14	CK108829	CK108829
C 99	14.4	49.7	67	29	CG487024	OST22337	CG487024	OST22337	C 172	14.2	49.0	74	29	CG667990	CG667990
C 100	14.4	49.7	67	29	CG487327	OST22793	CG487327	OST22793	C 173	14.2	49.0	75	9	AM100483	AM100483
C 101	14.4	49.7	67	29	CG487336	OST22805	CG487336	OST22805	C 174	14.2	49.0	75	29	CG618181	CG618181
C 102	14.4	49.7	67	29	CG487460	OST22970	CG487460	OST22970	C 175	14.2	49.0	75	29	BX176314	BX176314
C 103	14.4	49.7	67	29	CG487620	OST23207	CG487620	OST23207	C 176	14.2	49.0	76	28	BZ289518	BZ289518
C 104	14.4	49.7	67	29	CG487655	OST23250	CG487655	OST23250	C 177	14.2	49.0	79	28	AQ073107	AQ073107
C 105	14.4	49.7	67	29	CG488147	OST23952	CG488147	OST23952	C 178	14.2	49.0	34	29	TA98804P	TA98804P
C 106	14.4	49.7	67	29	CG488221	OST24055	CG488221	OST24055	C 179	14.2	49.0	42	28	BZ765887	BZ765887
C 107	14.4	49.7	67	29	CG488258	OST24096	CG488258	OST24096	C 180	14.2	49.0	54	10	BF643243	BF643243
C 108	14.4	49.7	67	29	CG488271	OST24115	CG488271	OST24115	C 181	14.2	49.0	58	29	BX156986	BX156986
C 109	14.4	49.7	67	29	CG488410	OST24338	CG488410	OST24338	C 182	14.2	49.0	64	10	BE588185	BE588185
C 110	14.4	49.7	67	29	CG488555	OST24524	CG488555	OST24524	C 183	14.2	49.0	65	29	FR0033439	FR0033439
C 111	14.4	49.7	67	29	CG489028	OST25301	CG489028	OST25301	C 184	14.2	49.0	67	9	AA936041	AA936041
C 112	14.4	49.7	67	29	CG489219	OST25655	CG489219	OST25655	C 185	14.2	49.0	67	9	AU265792	AU265792
C 113	14.4	49.7	67	29	CG489435	OST26024	CG489435	OST26024	C 186	14.2	49.0	67	14	CB261630	CB261630
C 114	14.4	49.7	67	29	CG489457	OST26071	CG489457	OST26071	C 187	14.2	49.0	71	29	CG646383	CG646383
C 115	14.4	49.7	67	29	CG489620	OST26373	CG489620	OST26373	C 188	14.2	49.0	72	28	CC458528	CC458528
C 116	14.4	49.7	67	29	CG489701	OST26526	CG489701	OST26526	C 189	14.2	49.0	76	9	AI633915	AI633915
C 117	14.4	49.7	67	29	CG489883	OST26861	CG489883	OST26861	C 190	14.2	49.0	80	29	AI797155	AI797155
C 118	14.4	49.7	67	29	CG490141	OST27215	CG490141	OST27215	C 191	14.2	49.0	80	29	AL943121	AL943121
C 119	14.4	49.7	67	29	CG490208	OST27304	CG490208	OST27304	C 192	13.8	47.6	27	2	HSM003610	HSM003610
C 120	14.4	49.7	67	29	CG490218	OST27317	CG490218	OST27317	C 193	13.8	47.6	30	2	HSM001042	HSM001042
C 121	14.4	49.7	67	29	CG490239	OST27347	CG490239	OST27347	C 194	13.8	47.6	30	2	HSM001581	HSM001581
C 122	14.4	49.7	67	29	CG490352	OST27476	CG490352	OST27476	C 195	13.8	47.6	30	28	AZ416940	AZ416940
C 123	14.4	49.7	67	29	CG490508	OST27693	CG490508	OST27693	C 196	13.8	47.6	32	2	HSM001595	HSM001595
C 124	14.4	49.7	67	29	CG490670	OST27894	CG490670	OST27894	C 197	13.8	47.6	32	2	HSM001674	HSM001674
C 125	14.4	49.7	67	29	CG490753	OST27998	CG490753	OST27998	C 198	13.8	47.6	33	2	HSM003086	HSM003086
C 126	14.4	49.7	67	29	CG490879	OST28161	CG490879	OST28161	C 199	13.8	47.6	33	9	AL048719	AL048719
C 127	14.4	49.7	67	29	CG490923	OST28228	CG490923	OST28228	C 200	13.8	47.6	33	9	AL048733	AL048733
C 128	14.4	49.7	67	29	CG490954	OST28265	CG490954	OST28265	C 201	13.8	47.6	34	2	HSM003069	HSM003069
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C 130	14.4	49.7	67	29	CG490976	OST28289	CG490976	OST28289	C 203	13.8	47.6	40	2	HSM001818	HSM001818
C 131	14.4	49.7	67	29	CG491020	OST28343	CG491020	OST28343	C 204	13.8	47.6	46	9	AA875851	AA875851
C 132	14.4	49.7	67	29	CG491291	OST28700	CG491291	OST28700	C 205	13.8	47.6	46	9	AA875851	AA875851
C 133	14.4	49.7	67	29	CG491363	OST28787	CG491363	OST28787	C 206	13.8	47.6	46	18	BH792322	BH792322
C 134	14.4	49.7	67	29	CG491379	OST28809	CG491379	OST28809	C 207	13.8	47.6	46	24	DI19975	DI19975
C 135	14.4	49.7	67	29	CG491411	OST28852	CG491411	OST28852	C 208	13.8	47.6	49	29	BX649704	BX649704
C 136	14.4	49.7	67	29	CG491434	OST28880	CG491434	OST28880	C 209	13.8	47.6	52	10	AW245287	AW245287
C 137	14.4	49.7	67	29	CG491452	OST28901	CG491452	OST28901	C 210	13.8	47.6	52	14	CD683281	CD683281
C 138	14.4	49.7	67	29	CG491456	OST28905	CG491456	OST28905	C 211	13.8	47.6	53	2	HSM002757	HSM002757
C 139	14.4	49.7	67	29	CG491618	OST29119	CG491618	OST29119	C 212	13.8	47.6	54	29	CC889004	CC889004
C 140	14.4	49.7	67	29	CG491850	OST29424	CG491850	OST29424	C 213	13.8	47.6	55	9	AI401076	AI401076
C 141	14.4	49.7	67	29	CG492124	OST29799	CG492124	OST29799	C 214	13.8	47.6	55	14	CB277382	CB277382
C 142	14.4	49.7	67	29	CG492151	OST29834	CG492151	OST29834	C 215	13.8	47.6	56	28	BH223717	BH223717
C 143	14.4	49.7	67	29	CG492636	OST27761	CG492636	OST27761	C 216	13.8	47.6	58	28	BH223717	BH223717
C 144	14.4	49.7	67	29	CG493157	OST31330	CG493157	OST31330	C 217	13.8	47.6	64	9	AI139668	AI139668
C 145	14.4	49.7	67	29	CG493162	OST31337	CG493162	OST31337	C 218	13.8	47.6	64	10	BF646978	BF646978
C 146	14.4	49.7	67	29	CG493452	OST31758	CG493452	OST31758	C 219	13.8	47.6	64	29	CG626740	CG626740
C 147	14.4	49.7	67	29	CG507869	OST58051	CG507869	OST58051	C 220	13.8	47.6	64	29	DR12A12S	DR12A12S
C 148	14.4	49.7	68	12	BG362185	GB52h02.Y	BG362185	GB52h02.Y	C 221	13.8	47.6	64	29	CG626740	CG626740
C 149	14.4	49.7	68	29	CG581901	OST222599	CG581901	OST222599	C 222	13.8	47.6	65	2	HSM001786	HSM001786
C 150	14.4	49.7	70	28	BH759592	KG052336-3	BH759592	KG052336-3	C 223	13.8	47.6	66	28	AZ781473	AZ781473

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C 245 13.6 46.9 63 29 CG475498
C 246 13.6 46.9 64 10 BG022449
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C 253 13.6 46.9 70 9 AI305284
C 254 13.6 46.9 71 12 BG271420
C 255 13.6 46.9 71 12 BG362349
C 256 13.6 46.9 71 29 CG512526
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C 268 13.4 46.2 34 28 BH50881
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C 288 13.4 46.2 71 12 BM873635
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C 368 13.2 45.5 72 28 BZ596806
C 369 13.2 45.5 74 9 AI819570

BM889450 laa01a12.
BH233862 1006176B1
EX653912 Arabidops
W99204 mf9512.r1
CG560534 O19181152
CG723421 1119076C1
AI569400 tn86b03.x
BG223022 nah41f05.
BG272656 nah35a08.
BG272660 nah35b06.
BQ287359 i166h08.x
BH910959 SALK_0636
BZ290283 SALK_0237
AI192699 ge67b01.x
AI300666 qo22a12.x
BG231398 nah42b02.
CG582886 OST224495
CG634017 OST234445
AL757078 Arabidops
BG222724 nah37g02.
BG231410 nah42c05.
BG272536 nah34d03.
BI494676 df112a06.
BG231456 nah42h01.
BG272005 nah16e09.
CB264027 95-E01502
CF249356 it72b03.Y
AZ441927 IM0234C22
CG573962 OST206260
AI560120 tq5a09.x
AW246447 28a1633.3
N86331 J7788F Huma
AZ993079 2M0277P20
AI057582 oy31c02.x
AI1378501 tc56h07.x
AZ817780 2M0087M23
AA935243 oo66f04.s
AZ317400 IM0036H20
AI758314 ty06c01.x
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AL487732 T. brucei
BF631974 NF007E11D
AZ494303 IM0329A03
BQ6785 CSRL-85e11-
BGI43998 ut86a06.x
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CA856138 PfESToac5
CC887033 SALK_1494
BE871815 601447803
BJ084264 BJ084264
BQ548512 rd12g10.Y
BM142363 if35e05.Y
BQ5670 CSRL-69f42-u
BG362434 gbt2b09.Y
CG563472 OST186777
AA939303 ol78g12.s
AU257206 AU257206
BX894767 Arabidops
AI019809 ua93c08.r
AI97603 70169x82
BX744082 BX744082
CB050259 NISC_gj16
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F30984 HSPD21789 H
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BZ596806 SALK_0960
AI819570 wj91g08.x

370	13.2	45.5	75	14	CK098783	A031P73.5	CK098783	A031P73.5	13	44.8	78	29	CG482517	OST15648
371	13.2	45.5	75	29	CG526082	OST102290	CG526082	OST102290	13	44.8	78	29	CG491713	OST29242
C 372	13.2	45.5	76	9	RA691060	v57b12.s	RA691060	v57b12.s	13	44.8	79	9	AA461918	vF95h10.r
C 373	13.2	45.5	76	9	AA938354	on71c08.s	AA938354	on71c08.s	13	44.8	79	12	BA314684	OP1.0.189
C 374	13.2	45.5	76	9	AA938354	on71c08.s	AA938354	on71c08.s	13	44.8	79	14	WA9294	mf62h03.r1
C 375	13.2	45.5	76	10	AW194637	AW194637	AW194637	AW194637	13	44.8	79	29	CG477179	OST96975.M
C 376	13.2	45.5	76	28	AZ482846	IM0308E08	AZ482846	IM0308E08	13	44.8	79	29	CG483993	OST17785
C 377	13.2	45.5	77	13	BU652110	1112097E1	BU652110	1112097E1	13	44.8	79	29	CG485151	OST19390
C 378	13.2	45.5	77	14	T474577	YC57c02.s1	T474577	YC57c02.s1	13	44.8	79	29	CG485511	OST19948
C 379	13.2	45.5	77	14	AF067770	AF067770	AF067770	AF067770	13	44.8	79	29	CG486032	OST20752
C 380	13.2	45.5	77	28	BH907776	SALK_0440	BH907776	SALK_0440	13	44.8	80	28	BH901319	SALK_0744
C 381	13.2	45.5	78	28	BH252197	SALK_0129	BH252197	SALK_0129	13	44.8	80	29	CG486056	OST20793
C 382	13.2	45.5	78	29	DR24P18T	DR24P18T	DR24P18T	DR24P18T	13	44.8	80	29	CG486056	ArabiDops
C 383	13.2	45.5	79	9	AA144854	mr73C08.r	AA144854	mr73C08.r	13	44.8	80	29	CG486056	ArabiDops
C 384	13.2	45.5	79	28	AZ828847	AZ828847	AZ828847	AZ828847	13	44.8	80	29	CG486056	ArabiDops
C 385	13.2	45.5	80	9	AJ499317	AJ499317	AJ499317	AJ499317	13	44.8	80	29	CG486056	ArabiDops
C 386	13.2	45.5	80	14	N36623	YX88d04.r1	N36623	YX88d04.r1	13	44.8	80	29	CG486056	ArabiDops
C 387	13.2	45.5	80	28	BZ357801	BZ357801	BZ357801	BZ357801	13	44.8	80	29	CG486056	ArabiDops
C 388	13	44.8	22	14	D18745	MUSGS01807	D18745	MUSGS01807	13	44.8	80	29	CG486056	ArabiDops
C 389	13	44.8	30	28	AZ780490	2M0017G24	AZ780490	2M0017G24	13	44.8	80	29	CG486056	ArabiDops
C 390	13	44.8	35	28	AL939013	ArabiDops	AL939013	ArabiDops	13	44.8	80	29	CG486056	ArabiDops
C 391	13	44.8	38	29	AG205629	Oryza sat	AG205629	Oryza sat	13	44.8	80	29	CG486056	ArabiDops
C 392	13	44.8	47	10	AW333805	S26D6 AGS	AW333805	S26D6 AGS	13	44.8	80	29	CG486056	ArabiDops
C 393	13	44.8	47	28	AZ622361	1M0459B09	AZ622361	1M0459B09	13	44.8	80	29	CG486056	ArabiDops
C 394	13	44.8	50	28	AZ622361	1M0459B09	AZ622361	1M0459B09	13	44.8	80	29	CG486056	ArabiDops
C 395	13	44.8	50	9	AU105337	AU105337	AU105337	AU105337	13	44.8	80	29	CG486056	ArabiDops
C 396	13	44.8	51	13	EQ593814	EQ593814	EQ593814	EQ593814	13	44.8	80	29	CG486056	ArabiDops
C 397	13	44.8	51	13	BI845578	f899g03.y	BI845578	f899g03.y	13	44.8	80	29	CG486056	ArabiDops
C 398	13	44.8	54	28	BH863662	SALK_0943	BH863662	SALK_0943	13	44.8	80	29	CG486056	ArabiDops
C 399	13	44.8	56	9	A1656187	A1656187	A1656187	A1656187	13	44.8	80	29	CG486056	ArabiDops
C 400	13	44.8	56	28	BZ382500	SALK_1183	BZ382500	SALK_1183	13	44.8	80	29	CG486056	ArabiDops
C 401	13	44.8	56	28	BZ382500	SALK_1183	BZ382500	SALK_1183	13	44.8	80	29	CG486056	ArabiDops
C 402	13	44.8	56	29	AL762058	ArabiDops	AL762058	ArabiDops	13	44.8	80	29	CG486056	ArabiDops
C 403	13	44.8	57	28	BH410651	1007019D1	BH410651	1007019D1	13	44.8	80	29	CG486056	ArabiDops
C 404	13	44.8	58	9	AA896470	AA896470	AA896470	AA896470	13	44.8	80	29	CG486056	ArabiDops
C 405	13	44.8	58	9	A1528594	A1528594	A1528594	A1528594	13	44.8	80	29	CG486056	ArabiDops
C 406	13	44.8	58	28	BH902709	BH902709	BH902709	BH902709	13	44.8	80	29	CG486056	ArabiDops
C 407	13	44.8	59	28	AZ800849	2M0059C02	AZ800849	2M0059C02	13	44.8	80	29	CG486056	ArabiDops
C 408	13	44.8	60	29	TA129G07P	TA129G07P	TA129G07P	TA129G07P	13	44.8	80	29	CG486056	ArabiDops
C 409	13	44.8	61	14	CD951024	SAT_319.G	CD951024	SAT_319.G	13	44.8	80	29	CG486056	ArabiDops
C 410	13	44.8	62	13	BQ265706	BQ265706	BQ265706	BQ265706	13	44.8	80	29	CG486056	ArabiDops
C 411	13	44.8	62	29	CG546868	OST168558	CG546868	OST168558	13	44.8	80	29	CG486056	ArabiDops
C 412	13	44.8	63	28	BH903683	SALK_0982	BH903683	SALK_0982	13	44.8	80	29	CG486056	ArabiDops
C 413	13	44.8	64	9	A1139668	qk28h07.x	A1139668	qk28h07.x	13	44.8	80	29	CG486056	ArabiDops
C 414	13	44.8	65	28	BH814721	BH814721	BH814721	BH814721	13	44.8	80	29	CG486056	ArabiDops
C 415	13	44.8	65	28	AZ346683	1M0082G05	AZ346683	1M0082G05	13	44.8	80	29	CG486056	ArabiDops
C 416	13	44.8	66	13	BQ761054	EBR004.SO	BQ761054	EBR004.SO	13	44.8	80	29	CG486056	ArabiDops
C 417	13	44.8	67	10	BF017439	BF017439	BF017439	BF017439	13	44.8	80	29	CG486056	ArabiDops
C 418	13	44.8	67	28	B01454	CSRL-131h3	B01454	CSRL-131h3	13	44.8	80	29	CG486056	ArabiDops
C 419	13	44.8	67	29	CG624461	OST32B242	CG624461	OST32B242	13	44.8	80	29	CG486056	ArabiDops
C 420	13	44.8	68	9	A1155708	ue03b12.r	A1155708	ue03b12.r	13	44.8	80	29	CG486056	ArabiDops
C 421	13	44.8	68	13	CG2494	HUMGS001238	CG2494	HUMGS001238	13	44.8	80	29	CG486056	ArabiDops
C 422	13	44.8	68	29	BX662822	ArabiDops	BX662822	ArabiDops	13	44.8	80	29	CG486056	ArabiDops
C 423	13	44.8	69	10	AW551533	L0080C08-	AW551533	L0080C08-	13	44.8	80	29	CG486056	ArabiDops
C 424	13	44.8	69	28	AZ662287	1M0541J16	AZ662287	1M0541J16	13	44.8	80	29	CG486056	ArabiDops
C 425	13	44.8	70	28	BH216023	1006039G0	BH216023	1006039G0	13	44.8	80	29	CG486056	ArabiDops
C 426	13	44.8	70	28	BZ354128	SALK_1232	BZ354128	SALK_1232	13	44.8	80	29	CG486056	ArabiDops
C 427	13	44.8	70	28	BZ768793	SALK_1407	BZ768793	SALK_1407	13	44.8	80	29	CG486056	ArabiDops
C 428	13	44.8	71	29	CG481208	OST13515	CG481208	OST13515	13	44.8	80	29	CG486056	ArabiDops
C 429	13	44.8	71	29	CG520678	OST85659	CG520678	OST85659	13	44.8	80	29	CG486056	ArabiDops
C 430	13	44.8	72	12	BJ082110	BJ082110	BJ082110	BJ082110	13	44.8	80	29	CG486056	ArabiDops
C 431	13	44.8	73	14	CK097081	UB38BFC12	CK097081	UB38BFC12	13	44.8	80	29	CG486056	ArabiDops
C 432	13	44.8	75	9	A1801746	co94n07.x	A1801746	co94n07.x	13	44.8	80	29	CG486056	ArabiDops
C 433	13	44.8	75	29	CG520478	CH240_367	CG520478	CH240_367	13	44.8	80	29	CG486056	ArabiDops
C 434	13	44.8	75	29	BX653572	ArabiDops	BX653572	ArabiDops	13	44.8	80	29	CG486056	ArabiDops
C 435	13	44.8	76	13	BQ548400	rd25h04.y	BQ548400	rd25h04.y	13	44.8	80	29	CG486056	ArabiDops
C 436	13	44.8	76	29	CG480684	OST12718	CG480684	OST12718	13	44.8	80	29	CG486056	ArabiDops
C 437	13	44.8	76	29	CG487317	OST22784	CG487317	OST22784	13	44.8	80	29	CG486056	ArabiDops
C 438	13	44.8	76	29	CG487318	lact28210.	CG487318	lact28210.	13	44.8	80	29	CG486056	ArabiDops
C 439	13	44.8	77	14	CF354398	CF354398	CF354398	CF354398	13	44.8	80	29	CG486056	ArabiDops
C 440	13	44.8	77	29	CG486552	OST121854	CG486552	OST121854	13	44.8	80	29	CG486056	ArabiDops
C 441	13	44.8	77	29	CG643392	CG643392	CG643392	CG643392	13	44.8	80	29	CG486056	ArabiDops
C 442	13	44.8	78	9	AA415010	vc50e05.r	AA415010	vc50e05.r	13	44.8	80	29	CG486056	ArabiDops

C 516	12.8	44.1	66	12	BG361575	BG361575	gb54h07.y	C 589	12.6	43.4	52	28	BZ662046	BZ662046	SALK_0255
C 517	12.8	44.1	66	12	BG361936	BG361936	gb49e12.y	C 590	12.6	43.4	53	12	BG315130	BG315130	POI_0.79
518	12.8	44.1	66	14	CB817611	CB817611	d3n12pz.f	591	12.6	43.4	53	28	BH852743	BH852743	SALK_0745
519	12.8	44.1	66	29	CG518752	CG518752	OST90980	592	12.6	43.4	53	29	EX660051	EX660051	Arabidops
C 520	12.8	44.1	66	29	TA123H02P	AL463084	T. brucei	593	12.6	43.4	54	9	AA506793	AA506793	EST031.Hu
C 521	12.8	44.1	67	9	AA506572	AA506572	n117407.s	594	12.6	43.4	55	10	AW698793	AW698793	r379 non-
C 522	12.8	44.1	67	14	CD946635	CD946635	REN_47.Ge	C 595	12.6	43.4	55	13	BU578287	BU578287	sa50h11.
C 523	12.8	44.1	67	28	BZ896657	BZ896657	SALK_0230	C 596	12.6	43.4	56	12	BU055025	BU055025	BM050525
C 524	12.8	44.1	68	12	BG409168	BG409168	gb87c02.y	C 597	12.6	43.4	56	28	AZ449951	AZ449951	IM0204K15
525	12.8	44.1	68	12	B1333307	B1333307	602996669	598	12.6	43.4	57	14	CB046012	CB046012	NISC_gf01
C 526	12.8	44.1	69	9	AA700612	AA700612	z141d03.s	599	12.6	43.4	57	28	AZ405121	AZ405121	IM0173020
527	12.8	44.1	69	10	AW698388	AW698388	G234.Glan	C 600	12.6	43.4	58	12	BM128723	BM128723	if15d09.y
C 528	12.8	44.1	69	29	CG793901	CG793901	SALK_0196	C 601	12.6	43.4	58	12	BM0509	BM0509	CSRL-115b2-
C 529	12.8	44.1	69	29	CG475794	CG475794	OST4390.M	C 602	12.6	43.4	60	9	AI1713784	AI1713784	as41b08.x
C 530	12.8	44.1	70	10	BF433300	BF433300	NF005B1E	C 603	12.6	43.4	61	9	AI189672	AI189672	qd3a08.x
C 531	12.8	44.1	70	13	C21062	C21062	HUMS000256	C 604	12.6	43.4	61	9	AA595454	AA595454	no34d06.s
C 532	12.8	44.1	70	14	CF033601	CF033601	QCH25h06.	C 605	12.6	43.4	61	9	AA612304	AA612304	vn97d10.r
533	12.8	44.1	70	29	CG718270	CG718270	1119052C0	606	12.6	43.4	61	10	BE248505	BE248505	NF006C12D
C 534	12.8	44.1	71	29	CG520384	CG520384	OST95614	C 607	12.6	43.4	61	29	CG513355	CG513355	OST96685
C 535	12.8	44.1	71	29	AA570253	AA570253	nf39e03.s	C 608	12.6	43.4	61	29	CG548659	CG548659	OST150666
C 536	12.8	44.1	72	10	BF460713	BF460713	UI-M-CGDP	C 609	12.6	43.4	62	10	AW638819	AW638819	bl75a04.w
C 537	12.8	44.1	72	10	BF462233	BF462233	UI-M-CGDP	C 610	12.6	43.4	62	29	CG474556	CG474556	OST2557.M
C 538	12.8	44.1	72	10	BF462877	BF462877	UI-M-CGDP	611	12.6	43.4	62	29	EX290641	EX290641	Arabidops
C 539	12.8	44.1	73	12	B1865610	B1865610	ft22h02.y	612	12.6	43.4	64	9	AA748758	AA748758	ny06h06.s
C 540	12.8	44.1	73	13	BQ128805	BQ128805	ii23c08.y	C 613	12.6	43.4	64	9	AI584516	AI584516	fb95a02.x
541	12.8	44.1	73	13	BQ128805	BQ128805	ii23c031A0	C 614	12.6	43.4	64	10	BF118530	BF118530	SMOVL3CAN
542	12.8	44.1	73	29	CG778959	CG778959	ii23c031A0	C 615	12.6	43.4	64	12	BM515149	BM515149	k165a07.y
C 543	12.8	44.1	74	9	AA574536	AA574536	vm29e03.x	C 616	12.6	43.4	64	29	AG265379	AG265379	Lotus cor
544	12.8	44.1	74	13	BQ265575	BQ265575	NISC_ff07	C 617	12.6	43.4	65	9	AG620913	AG620913	af96b03.s
545	12.8	44.1	74	13	BQ591165	BQ591165	S013311-0	C 618	12.6	43.4	65	14	CF885082	CF885082	tr1c077Kh
546	12.8	44.1	74	13	BU672599	BU672599	ha98002x1	C 619	12.6	43.4	65	28	BH810688	BH810688	SALK_0510
C 547	12.8	44.1	74	28	AZ918214	AZ918214	1006003F0	620	12.6	43.4	65	29	CG708273	CG708273	1119008C1
C 548	12.8	44.1	74	28	CG202432	CG202432	3591.1.2	621	12.6	43.4	66	14	CB053335	CB053335	NISC_g113
549	12.8	44.1	74	29	CG581504	CG581504	OST211848	622	12.6	43.4	66	28	AZ500141	AZ500141	IM0338016
C 550	12.8	44.1	75	12	BG361021	BG361021	qb44e08.y	623	12.6	43.4	67	14	CB165153	CB165153	86 Al.falf
C 551	12.8	44.1	76	9	AV560198	AV560198	AV560198	624	12.6	43.4	67	14	CB357125	CB357125	ZF001-P00
C 552	12.8	44.1	76	29	CG536220	CG536220	OST360383	625	12.6	43.4	67	14	CF278112	CF278112	14FTL-03
553	12.8	44.1	76	29	CG565682	CG565682	OST429400	C 626	12.6	43.4	67	29	AA543322	AA543322	OST139031
554	12.8	44.1	77	9	AA037767	AA037767	mc10h01.r	C 627	12.6	43.4	68	9	AG826444	AG826444	oe66a01.s
C 555	12.8	44.1	77	13	BQ243044	BQ243044	TaE15019H	628	12.6	43.4	68	10	AW552311	AW552311	L0212D01-
C 556	12.8	44.1	77	13	BQ244040	BQ244040	TaE15005F	629	12.6	43.4	68	29	CG730236	CG730236	1119123D0
C 557	12.8	44.1	77	14	CG562321	CG562321	66-B8867-	630	12.6	43.4	69	12	BG271713	BG271713	na152f03.
C 558	12.8	44.1	77	29	AG258132	AG258132	Lotus cor	631	12.6	43.4	69	28	AZ818727	AZ818727	2M0088K22
559	12.8	44.1	78	9	AA415410	AA415410	VD02f07.s	632	12.6	43.4	70	9	AI536249	AI536249	vg99e07.x
C 560	12.8	44.1	78	10	BG633280	BG633280	H305C03-	C 633	12.6	43.4	70	9	AI644963	AI644963	vs48h01.y
C 561	12.8	44.1	78	10	AW443383	AW443383	AB510.Pri	C 634	12.6	43.4	70	13	BU063954	BU063954	Fgr_3.M18
C 562	12.8	44.1	78	14	CD953730	CD953730	SBK_48.Ge	635	12.6	43.4	70	29	CG545898	CG545898	OST143669
C 563	12.8	44.1	78	14	CD953937	CD953937	SBM_106.G	636	12.6	43.4	71	28	AZ591297	AZ591297	IM0401014
C 564	12.8	44.1	78	28	BZ379882	BZ379882	SALK_1141	637	12.6	43.4	72	10	AW173647	AW173647	x110d06.x
C 565	12.8	44.1	78	29	CG473421	CG473421	OST858.Mu	638	12.6	43.4	72	12	BG793538	BG793538	UTSW_SML3
C 566	12.8	44.1	79	9	AI271934	AI271934	q188f04.x	639	12.6	43.4	72	14	T25592	T25592	EST00628.Un
C 567	12.8	44.1	79	29	CG604315	CG604315	OST279865	640	12.6	43.4	72	29	CG666004	CG666004	OST455530
C 568	12.8	44.1	79	29	AL760717	AL760717	Arabidops	C 641	12.6	43.4	73	10	BF400538	BF400538	SMOVL3CAN
569	12.8	44.1	80	29	BX783166	BX783166	EX783166	642	12.6	43.4	73	14	CB817159	CB817159	d3a21pz.f
C 570	12.8	44.1	80	29	CG574141	CG574141	OST206705	C 643	12.6	43.4	73	29	CG529491	CG529491	OST109956
C 571	12.6	43.4	25	28	AZ766828	AZ766828	IM0569C06	644	12.6	43.4	74	14	CD673927	CD673927	fg05g01.x
C 572	12.6	43.4	27	29	CG723079	CG723079	1119074P0	645	12.6	43.4	74	14	CF651628	CF651628	10-L02016
C 573	12.6	43.4	29	28	BH666445	BH666445	SALK_1013	646	12.6	43.4	74	28	BZ595894	BZ595894	SALK_0897
C 574	12.6	43.4	32	28	AZ929242	AZ929242	2M0277G18	647	12.6	43.4	74	29	CG597517	CG597517	OST261044
C 575	12.6	43.4	35	9	AU256066	AU256066	AU256066	C 648	12.6	43.4	75	9	AI254006	AI254006	qv34d09.x
C 576	12.6	43.4	35	9	AU252527	AU252527	AU252527	C 649	12.6	43.4	75	9	AI345051	AI345051	tb01h03.x
577	12.6	43.4	39	28	BH840522	BH840522	KG03386-5	C 650	12.6	43.4	75	9	AJ444040	AJ444040	AJ444040
578	12.6	43.4	39	28	BH405111	BH405111	Arabidops	C 651	12.6	43.4	75	12	BM571633	BM571633	fx04a07.x
579	12.6	43.4	48	10	AW45085	AW45085	2819816.3	652	12.6	43.4	75	28	B46656	B46656	HS-1065-B1-
C 581	12.6	43.4	50	9	CF779665	CF779665	AL779665	C 653	12.6	43.4	75	28	BZ382121	BZ382121	SALK_1178
C 582	12.6	43.4	50	14	CF291606	CF291606	14ROOT--0	C 654	12.6	43.4	76	9	AI625418	AI625418	ty54h12.x
C 583	12.6	43.4	51	28	AZ582371	AZ582371	IM0374A17	655	12.6	43.4	76	13	BQ391463	BQ391463	NISC_mq18
C 584	12.6	43.4	51	28	B01106	B01106	CSRL-125g12	656	12.6	43.4	76	14	CB817534	CB817534	d3111pz.f
C 585	12.6	43.4	52	9	AA918429	AA918429	o170h08.s	657	12.6	43.4	76	28	BZ288764	BZ288764	SALK_0221
C 586	12.6	43.4	52	10	AW686481	AW686481	NF038E05N	C 658	12.6	43.4	77	9	AV847346	AV847346	AV847346
587	12.6	43.4	52	28	AZ308266	AZ308266	IM0011N04	659	12.6	43.4	77	10	AW246812	AW246812	2822428.3
588	12.6	43.4	52	28	B06941	B06941	CSRL-88F4-u	661	12.6	43.4	77	14	CF013238	CF013238	QBK3e08.x

662	12.6	43.4	77	14	CF307808	ABF--01-F	CF307808	ABF--01-F	61	29	CG513867	OST67472
663	12.6	43.4	77	28	A2480103	1M0301A22	A2480103	1M0301A22	62	29	BX892075	ArabiDops
664	12.6	43.4	77	29	CG608441	OST288586	CG608441	OST288586	63	29	AI7271280	QW83R01.X
665	12.6	43.4	77	29	AL949179	ArabiDops	AL949179	ArabiDops	63	28	BX597224	SALK_1005
666	12.6	43.4	78	9	AI633270	ng58b02.s	AI633270	ng58b02.s	64	9	AU053942	AU053942
667	12.6	43.4	78	9	AI494846	sb05b07.Y	AI494846	sb05b07.Y	64	12	BI330183	602983809
668	12.6	43.4	78	12	BJ059307	BJ059307	BJ059307	BJ059307	64	28	AZ433678	1M0219007
669	12.6	43.4	79	9	AA097644	mm36e12.r	AA097644	mm36e12.r	64	28	AL751853	ArabiDops
670	12.6	43.4	79	9	AA336213	n182d01.s	AA336213	n182d01.s	65	9	AI281558	qu52902.X
671	12.6	43.4	79	13	BQ582546	E012279-0	BQ582546	E012279-0	65	13	BX744236	BX744236
672	12.6	43.4	79	28	CC041610	3591_114	CC041610	3591_114	65	29	CG662550	OST446737
673	12.6	43.4	79	29	AL951473	ArabiDops	AL951473	ArabiDops	66	28	AZ400381	1M0166G08
674	12.6	43.4	79	29	BX656286	ArabiDops	BX656286	ArabiDops	66	28	AZ492869	1M0227B13
675	12.6	43.4	80	14	CF313886	HD--10-J0	CF313886	HD--10-J0	66	29	CG584009	OST226784
676	12.6	43.4	80	14	CF331598	NACL--07-	CF331598	NACL--07-	66	29	CG696248	BARC_BFGL
677	12.6	43.4	80	14	CF331599	NACL--07-	CF331599	NACL--07-	66	29	CG696248	BARC_BFGL
678	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	TA118805P	
679	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
680	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
681	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
682	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
683	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
684	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
685	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
686	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
687	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
688	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
689	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
690	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
691	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
692	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
693	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
694	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
695	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
696	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
697	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
698	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
699	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
700	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
701	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
702	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
703	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
704	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
705	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
706	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
707	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
708	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
709	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
710	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
711	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
712	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
713	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
714	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
715	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
716	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
717	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
718	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
719	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
720	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
721	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
722	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
723	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
724	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
725	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
726	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
727	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
728	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
729	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
730	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
731	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
732	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
733	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s
734	12.6	43.4	80	29	CG611871	OSP111917	CG611871	OSP111917	67	29	AA894821	Oj61d12.s

C 808	12.4	42.8	79	10	AW395388	sh48d12.1
C 809	12.4	42.8	79	12	B1703865	rm03a05.Y
C 810	12.4	42.8	79	14	CD682985	ij29a04.Y
C 811	12.4	42.8	79	29	AL948895	ArabiIdops
C 812	12.4	42.8	79	29	EX004713	ArabiIdops
C 813	12.4	42.8	80	10	BG021609	dg33b06.X
C 814	12.4	42.8	80	14	CF331113	NACL--07-
C 815	12.4	42.8	80	28	BH230335	1006157D0
C 816	12.2	42.1	20	28	A2451921	1M0251C05
C 817	12.2	42.1	21	2	HSM001528	Homo sapi
C 818	12.2	42.1	25	2	HSM001707	Homo sapi
C 819	12.2	42.1	25	28	AZ851359	Homo sapi
C 820	12.2	42.1	26	28	AZ303394	1M0003J22
C 821	12.2	42.1	26	28	BZ664493	SALK_0756
C 822	12.2	42.1	27	28	BZ380070	SALK_1145
C 823	12.2	42.1	28	2	HSM001758	Homo sapi
C 824	12.2	42.1	28	2	HSM003578	Homo sapi
C 825	12.2	42.1	29	2	HSM001333	Homo sapi
C 826	12.2	42.1	29	2	HSM002271	Homo sapi
C 827	12.2	42.1	29	2	HSM002384	Homo sapi
C 828	12.2	42.1	29	2	HSM003053	Homo sapi
C 829	12.2	42.1	29	2	HSM003484	Homo sapi
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C 831	12.2	42.1	29	28	AZ345451	1M0080112
C 832	12.2	42.1	30	2	HSM001432	Homo sapi
C 833	12.2	42.1	30	2	HSM001590	Homo sapi
C 834	12.2	42.1	30	2	HSM001698	Homo sapi
C 835	12.2	42.1	30	2	HSM002253	Homo sapi
C 836	12.2	42.1	30	2	HSM003231	Homo sapi
C 837	12.2	42.1	30	2	HSM003322	Homo sapi
C 838	12.2	42.1	30	2	HSM003483	Homo sapi
C 839	12.2	42.1	30	2	HSM003500	Homo sapi
C 840	12.2	42.1	30	9	AL048796	DKF2p566P
C 841	12.2	42.1	31	2	HSM002270	Homo sapi
C 842	12.2	42.1	31	2	HSM003327	Homo sapi
C 843	12.2	42.1	31	9	AA910965	OK67a10.1S
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C 849	12.2	42.1	32	9	AL036826	DKF2p564M
C 850	12.2	42.1	33	2	HSM001190	Homo sapi
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C 852	12.2	42.1	33	28	AZ316652	1M0034E23
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55	28	BA5176	HS-1060	Bapi
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58	10	AW333702	AW333702	S25A3 AGS
58	14	CA850023	CA850023	k118e09.y
58	14	CA850023	CA850023	k118e09.y
58	28	AZ499503	AZ499503	1M0337M13
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64	9	A12711399	A12711399	gw82e01.x
64	9	A12711399	A12711399	gw82e01.x
64	9	A1305424	A1305424	gw77a04.x
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C 960	12.2	42.1	64	28	BG650851	BH903232 SALK_1022
C 961	12.2	42.1	64	29	EX231457	CG650851 OST409780
C 962	12.2	42.1	65	9	AL884705	EX231457 Arabidops
C 963	12.2	42.1	65	9	AU053940	AL884705 AL884705
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C 966	12.2	42.1	65	29	CNS03K4G	CF045820 QCK18d07.
C 967	12.2	42.1	66	9	A1571487	CF45820 Tetraodon
C 968	12.2	42.1	66	9	AL898170	A1571487 trt56g10.x
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C 975	12.2	42.1	66	28	BZ663467	BH904510 SALK_1045
C 976	12.2	42.1	66	29	AL762061	BZ663467 SALK_0270
C 977	12.2	42.1	67	9	A1423689	AL762061 Arabidops
C 978	12.2	42.1	67	9	A1798755	A1423689 tf85f06.x
C 979	12.2	42.1	67	14	CA334775	A1798755 wa92c05.x
C 980	12.2	42.1	67	14	CA335215	CA334775 NISC_lt01
C 981	12.2	42.1	67	29	EX004510	CA335215 NISC_lt07
C 982	12.2	42.1	67	29	TA176H08Q	EX004510 Arabidops
C 983	12.2	42.1	68	9	A1348734	TA176H08Q trt.brucei
C 984	12.2	42.1	68	9	AA551800	A1348734 ta83dl12.x
C 985	12.2	42.1	68	14	CB261164	AA551800 nk04a12.s
C 986	12.2	42.1	68	14	CB353381	CB261164 23-E9407-s
C 987	12.2	42.1	68	28	AZ779515	CB353381 ZF001-P00
C 988	12.2	42.1	68	28	BZ288968	AZ779515 2M0016106
C 989	12.2	42.1	68	29	CG547926	BZ288968 SALK_0223
C 990	12.2	42.1	69	12	BG943637	CG547926 OST149074
C 991	12.2	42.1	69	12	BW023345	BG943637 ax27g06.x
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C 993	12.2	42.1	69	14	CA336899	CA335433 NISC_lt11
C 994	12.2	42.1	69	14	CD712860	CA336899 NISC_lv06
C 995	12.2	42.1	69	14	CD922033	CD712860 VVB016H01
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C 998	12.2	42.1	69	29	BX530939	CG516082 OST73926
C 999	12.2	42.1	70	9	AI308361	BX530939 Arabidops
1000	12.2	42.1	70	9	AI337589	AI308361 tb43a05.x AI337589 qw91a07.x

ALIGNMENTS

RESULT 1	70 bp mRNA linear EST 14-JUL-1997
LOCUS AA516989/c	
DEFINITION vhs9d02.r1 Knowles Solter mouse embryonic stem cell Mus musculus	
KEYWORDS cDNA clone IMAGE:594147 5' similar to TR:G187568 GI87568 MG44 ;,	
SOURCE mRNA sequence.	
ACCESSION AA516989	
VERSION AA516989.1	GI:2256448
KEYWORDS EST.	
SOURCE Mus musculus (house mouse)	
ORGANISM Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
1 (bases 1 to 70)	
Marra,M., Haller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,	
Gaisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,B.,	
Schellenberg,K., Steptoe	


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/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/note="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGATTTCGGCGCGCTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

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ORIGIN

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Query Match          60.0%; Score 17.4; DB 9; Length 67;
Best Local Similarity 55.8%; Pred. No. 3e+04; 6; Indels 0; Gaps 0;
Matches 15; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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QY 3 AGAUCUUUUUUAAGCCCAAGGCU 29
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Db 51 AGAGACTTCTTGTAACCCCAAGGCT 25

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RESULT 3

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AI609394/c
LOCUS AI609394 70 bp mRNA linear EST 16-DEC-1999
DEFINITION tw93b03.x1 NCI_CGAP_HN6 Homo sapiens cDNA clone IMAGE:2267213 3' similar to SW:TCFH_HUMAN Q99832 T-COMPLEX PROTEIN 1, ETA SUBUNIT 1, mRNA sequence.
ACCESSION AI609394 GI:4618561
VERSION EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 70)
REFERENCE NCI/MDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute / National Institute of Dental Research, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Chong Heon Lee, D.D.S., Mary May, J. Silvio Gutkind, Ph.D., Myung Hee Park, Ph.D.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

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Trace considered overall poor quality
Insert Length: 2028 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
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/clone="IMAGE:2267213"
/tissue_type="normal gingiva (cell line from immortalized keratinocytes)"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="NCI_CGAP_HN6"

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FEATURES

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/db_xref="taxon:9606"
/clone="IMAGE:2267213"
/tissue_type="normal gingiva (cell line from immortalized keratinocytes)"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="NCI_CGAP_HN6"

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/note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. 5' adaptor sequence: 5' AATTCGCGACGAG 3' GCGGCTC 5' 3' adaptor sequence: 5' (GA)10ACTAGTCGAGTTT 3' EcoRI site appears to have been lost in a fraction of the clones. Library constructed by Stratagene; available through Mary May, PhD (Oral and Pharyngeal Cancer Branch, National Institute of Dental and Craniofacial Research, NIH; mmayyoda.nidcr.nih.gov)."

```

ORIGIN

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Query Match          57.2%; Score 16.6; DB 9; Length 70;
Best Local Similarity 47.8%; Pred. No. 5.9e+04;
Matches 11; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

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QY 6 UCUUUUUGUAGCCCAAGGCC 28
    : : : : : ||| : ||| : ||| :
Db 54 TTTTGTGTGGGCCCAAGGCC 32

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RESULT 4

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H07686/c
LOCUS H07686 75 bp mRNA linear EST 23-JUN-1995
DEFINITION Kgs012 BNLI Brassica napus cDNA 3', mRNA sequence.
ACCESSION H07686
VERSION EST.
KEYWORDS H07686.1 GI:872508
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 75)
REFERENCE Sohn,U., Lee,C.M., Cho,K.H., Jeon,Y.H., Hahn,T.R. and Nam,H.G.
AUTHORS cDNAs from Brassica napus (rape)
TITLE Unpublished (1995)
JOURNAL Contact: Uik Sohn
COMMENT Laboratory of Molecular Biology
Kyungpook National University
Dept. of Genetic Eng., Kyungpook National Univ., Taegu 702-701, Korea
Tel: 0539505382
Fax: 0539555327
Email: usohn@bh.kyungpook.ac.kr
EST is putatively homologous to unknown gene
Seq primer: M13 forward.

```

FEATURES

```

source
1..75
/organism="Brassica napus"
/mol_type="mRNA"
/strain="cv. Naehan"
/db_xref="taxon:3708"
/lab_host="NMS22"
/clone_lib="BNLI"
/note="Vector: pT7T3D; Site 1: NotI; Site 2: EcoRI; Poly(A)-mRNA was purified from the leaf of B.napus. cDNA library was constructed from the mRNAs by oligo(dT) priming and directionally cloned from the NotI site in the vector pT7T3D (Pharmacia) to the EcoRI site."

```

ORIGIN

```

Query Match          57.2%; Score 16.6; DB 14; Length 75;
Best Local Similarity 56.5%; Pred. No. 5.9e+04;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

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QY 7 UCUUUUUGUAGCCCAAGGCCU 29
    : : : : : ||| : ||| : ||| :
Db 34 TCTTCTTGAAGCTCAAGGCT 12

```

RESULT 5

```

BG361927/c
LOCUS BG361927 51 bp mRNA linear EST 08-MAR-2001

```

DEFINITION gb49d10.y1 Moss EST library PPG Physcomitrella patens cDNA clone
 PEP_SOURCE_ID: 5', mRNA sequence.
 ACCESSION BG361927
 VERSION BG361927.1 GI:13251024
 KEYWORDS EST.
 SOURCE Physcomitrella patens
 ORGANISM Physcomitrella patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
 1 (Bases 1 to 51)
 REFERENCE Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C.,
 Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,
 Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,
 Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E.,
 Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
 Leeds/Wash U Moss EST Project
 Unpublished (1999)
 TITLE Contact: Ralph Quatrano
 JOURNAL Leeds/Wash U Moss EST Project
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Libraries were constructed by Dr. Stavros Bashardes as part of the
 Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
 Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1..51
 /organism="Physcomitrella patens"
 /mol_type="mRNA"
 /db_xref="taxon:3218"
 /clone="PEP_SOURCE_ID:"
 /tissue_type="gametophore: 30 day old tissue,
 ammonium-grown"
 /lab_host="DH10B"
 /clone_lib="Moss EST library PPG"
 /note="Vector: pAMP1; Construction of the cDNA library was
 performed by Dr. W. Gregg Clark using a modification of
 the cDNA synthesis protocol developed in the laboratory of
 Dr. Michael Lovett by Dr. Yulia Korshunova (personal
 communication). First polyA + RNA was isolated from total
 gametophore RNA using oligo dT magnetic beads. Following
 this, first strand cDNA synthesis was performed on the
 bead-bound polyA + RNA, during which an oligonucleotide
 anchor sequence was incorporated onto the 5'-ends of the
 cDNA. PCR amplification was then used to synthesize the
 second strand to amplify the double stranded DNA, and to
 incorporate dUTP containing sequences into the ends of the
 double stranded cDNA. This DNA was size selected and
 cloned into pAMP1 using the CloneAMP PAMPI System (Life
 Technologies, GibcoBRL) for cloning amplification products
 by a non-restriction site dependant process. The cloning
 was directional based on sequence asymmetry introduced at
 the ends during PCR amplification. The 3' cDNA ends are
 proximal to the NotI site of the multiple cloning site in
 pAMP1. This annealing mixture was transformed into
 chemically competent DH10B cells and selected for
 ampicillin resistant growth. The resulting clones (about
 330,000) were pooled to make the library."
 ORIGIN
 Query Match 55.2%; Score 16; DB 12; Length 51;
 Best Local Similarity 41.7%; Pred. No. 1.1e+05; Indels 0; Gaps 0;
 Matches 10; Conservative 9; Mismatches 5;
 QY 6 UUCUUUUGUAGCCCAAGGCU 29
 :: ::::: ||| ||||| |:
 Db 27 TTTTITTTTAAAGCCCAAGACT 4

RESULT 6
 BG361878/73 bp mRNA linear EST 08-MAR-2001
 LOCUS GB46B10.y1 Moss EST library PPG Physcomitrella patens cDNA clone
 DEFINITION PEP_SOURCE_ID: 5', mRNA sequence.
 ACCESSION BG361878
 VERSION BG361878.1 GI:13250975
 KEYWORDS EST.
 SOURCE Physcomitrella patens
 ORGANISM Physcomitrella patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
 1 (Bases 1 to 73)
 REFERENCE Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C.,
 Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,
 Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,
 Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E.,
 Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
 Leeds/Wash U Moss EST Project
 Unpublished (1999)
 TITLE Contact: Ralph Quatrano
 JOURNAL Leeds/Wash U Moss EST Project
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Libraries were constructed by Dr. Stavros Bashardes as part of the
 Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
 Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1..73
 /organism="Physcomitrella patens"
 /mol_type="mRNA"
 /db_xref="taxon:3218"
 /clone="PEP_SOURCE_ID:"
 /tissue_type="gametophore: 30 day old tissue,
 ammonium-grown"
 /lab_host="DH10B"
 /clone_lib="Moss EST library PPG"
 /note="Vector: pAMP1; Construction of the cDNA library was
 performed by Dr. W. Gregg Clark using a modification of
 the cDNA synthesis protocol developed in the laboratory of
 Dr. Michael Lovett by Dr. Yulia Korshunova (personal
 communication). First polyA + RNA was isolated from total
 gametophore RNA using oligo dT magnetic beads. Following
 this, first strand cDNA synthesis was performed on the
 bead-bound polyA + RNA, during which an oligonucleotide
 anchor sequence was incorporated onto the 5'-ends of the
 cDNA. PCR amplification was then used to synthesize the
 second strand to amplify the double stranded DNA, and to
 incorporate dUTP containing sequences into the ends of the
 double stranded cDNA. This DNA was size selected and
 cloned into pAMP1 using the CloneAMP PAMPI System (Life
 Technologies, GibcoBRL) for cloning amplification products
 by a non-restriction site dependant process. The cloning
 was directional based on sequence asymmetry introduced at
 the ends during PCR amplification. The 3' cDNA ends are
 proximal to the NotI site of the multiple cloning site in
 pAMP1. This annealing mixture was transformed into
 chemically competent DH10B cells and selected for
 ampicillin resistant growth. The resulting clones (about
 330,000) were pooled to make the library."
 ORIGIN
 Query Match 55.2%; Score 16; DB 12; Length 73;
 Best Local Similarity 45.8%; Pred. No. 9.9e+04; Indels 0; Gaps 0;
 Matches 11; Conservative 8; Mismatches 5;

```

Qy 6 UUUUUUUUUAAGCCCAAGGCU 29
Db 40 TTTTGGAGAGCCCAAGACT 17

RESULT 7
AI824019/c
LOCUS
DEFINITION
w329f03.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2404253 3'
similar to TR:070278 070278 MULTIPLE ENDOCRINE NEOPLASIA TYPE 1
CANDIDATE PROTEIN NUMBER 18. ; mRNA sequence.
AI824019
VERSION
AI824019.1 GI:5444690
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 58)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 806 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..58
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2404253"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid12"
/notes="Organ: kidney; Vector: pT7T3D-pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kids was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Fatima Bonaldo."

ORIGIN
Query Match 54.5%; Score 15.8; DB 9; Length 58;
Best Local Similarity 44.4%; Pred. No. 1.2e+05;
Matches 12; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 3 AGAUUUUUUUAAGCCCAAGGCU 29
Db 56 AGCTTTTTCCTCAAGTCCAAAGAGCT 30

RESULT 8
BQ613481/c
LOCUS
DEFINITION
BQ613481
rd07h06.y1 Meloidogyne incognita egg SL1 TOPO VI Meloidogyne
incognita cDNA 5', mRNA sequence.

ORIGIN
Query Match 54.5%; Score 15.8; DB 9; Length 58;
Best Local Similarity 44.4%; Pred. No. 1.2e+05;
Matches 12; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 9 UUUUUUUAAGCCCAAGG 27
Db 47 TTTTCTAAGCCCAAGG 29

RESULT 9
AZ657549
LOCUS
DEFINITION
AZ657549
1M0533118R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0533118 R, genomic survey sequence.
AZ657549
VERSION
AZ657549.1 GI:11794695
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 76)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Famil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

ACCESSION
BQ613481
VERSION
BQ613481.1 GI:21603157
KEYWORDS
SOURCE
EST.
ORGANISM
Meloidogyne incognita (southern root-knot nematode)
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
1 (bases 1 to 72)
McCartter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagaris, V., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Watterton, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
TITLE
The Washington Univ. Nematode EST Project, 1999
JOURNAL
COMMENT
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCartter
at Washington University, St. Louis. Meloidogyne incognita eggs
were provided by Andrew Kloek of Divergence Inc., St. Louis, MO.
Putative full length read
The vector to vector length is 73
Seq primer: -40RP from Gibco.
Location/Qualifiers
1..72
/organism="Meloidogyne incognita"
/mol_type="mRNA"
/db_xref="taxon:6306"
/dev_stage="egg"
/lab_host="DH10B (Invitrogen)"
/clone_lib="Meloidogyne incognita egg SL1 TOPO v1"
/notes="Vector: pCR11-TOPO (Invitrogen); Site 1: EcoRI;
Site 2: EcoRI; The library was constructed by Claire
Murphy and Dr. James McCartter at Washington University,
St. Louis. Oligo (dT)-SL1 PCR based library. cDNA PCR
products of size >400 nucleotides containing SL1 on the 5'
end and oligo(dT) on the 3' end were non-directionally
cloned into pCR11-TOPO (Invitrogen) following the TOPO TA
cloning protocol. Meloidogyne incognita eggs were provided
by Andrew Kloek of Divergence Inc., St. Louis, MO."

ORIGIN
Query Match 54.5%; Score 15.8; DB 13; Length 72;
Best Local Similarity 57.9%; Pred. No. 1.2e+05;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 9 UUUUUUUAAGCCCAAGG 27
Db 47 TTTTCTAAGCCCAAGG 29

RESULT 9
AZ657549
LOCUS
DEFINITION
AZ657549
1M0533118R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0533118 R, genomic survey sequence.
AZ657549
VERSION
AZ657549.1 GI:11794695
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 76)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Famil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

```

TITLE
JOURNAL
COMMENT

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0533 row: L column: 18
 Seq primer: CACACAGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 76.
 Location/Qualifiers
 1. 76
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /dd_xref="taxon:10090"
 /clone="UGCIN0533L18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UGCIM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (G1473114|GB|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 54.5%; Score 15.8; DB 28; Length 76;
 Best Local Similarity 44.4%; Pred. No. 1.2e+05;
 Matches 12; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 3 AGAUCUUUUUUAAGCCCAAGGCU 29
 |||:|||||:|||||:|||||:
Db 43 AGTTCTTTTGGAGGCACTCAGACT 69
 |||:|||||:|||||:|||||:

RESULT 10
AI802260
LOCUS
DEFINITION
 t336907.x1 NCI CGAP Panel Homo sapiens cDNA clone IMAGE:2143644 3'
 similar to TR:Q41120 Q41120 HYDROXYPROLINE-RICH GLYCOPROTEIN ;,
 mRNA sequence.

ACCESSION
AI802260
VERSION
AI802260.1 GI:5367732
KEYWORDS
SOURCE
ORGANISM
 Homo sapiens (human)
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 37)
REFERENCE
AUTHORS
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE
JOURNAL
COMMENT

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: sgabbs@email.nih.gov
 Life Technologies catalog #: 11548-013
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

FEATURES
source
 1. 37
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2143644"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Panel"
 /notes="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

ORIGIN

Query Match 53.8%; Score 15.6; DB 9; Length 37;
 Best Local Similarity 50.8%; Pred. No. 1.6e+05;
 Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AAGAUCUUUUUUAAGGCCCC 22
 |||:|||||:|||||:|||||:
Db 7 AAAATTTTITTTTGAAGCCCC 28
 |||:|||||:|||||:|||||:

RESULT 11
A2834846/c
LOCUS
DEFINITION
 2M0117F18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0117F18 R, genomic survey sequence.

ACCESSION
A2834846
VERSION
A2834846.1 GI:13004754
KEYWORDS
SOURCE
ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 58)
REFERENCE
AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0117 row: F column: 18
 Seq primer: CACACAGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 58.
 Location/Qualifiers


```

survey sequence.
ACCESSION AG260396
VERSION AG260396.1 GI:26660233
KEYWORDS GSS.
SOURCE Locus corniculatus var. japonicus (Locus japonicus)
ORGANISM Locus corniculatus var. japonicus
REFERENCE Sato, S., Nakamura, Y. and Tabata, S.
AUTHORS Locus japonicus TAC End sequences
TITLE Published Only in Database (2002)
JOURNAL
REFERENCE Sato, S.
AUTHORS Locus corniculatus var. japonicus
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: ssato@kazusa.or.jp; URL: http://www.kazusa.or.jp/en/plant/,
Tel: 81-438-52-3935 (ex.2336), Fax: 81-438-52-3934)
FEATURES
Location/Qualifiers
1..78
source
/mol_type="genomic DNA"
/strain="Wiyakojima MG-20"
/variety="japonicus"
/db_xref="taxon:34305"
/clone="LjT50h16_sfi"
/clone_lib="genomic TAC library"
/note="VECTOR: pYL7AC7-synonym: Locus japonicus"

ORIGIN
Query Match 53.1%; Score 15.4; DB 29; Length 78;
Best Local Similarity 58.8%; Pred. No. 1.6e+05;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 9 UUUUGUAGCCCAAG 25
Db 22 TTTTGTAGACCCAG 6

RESULT 15
AI318033
LOCUS
DEFINITION ta75902 x1 NCI CGAP HSC2 Homo sapiens cDNA clone IMAGE:2049938 3'
similar to SW1RL34_HUMAN P49207 60S RIBOSOMAL PROTEIN L34. ; mRNA
sequence.
ACCESSION AI318033
VERSION AI318033.1 GI:4033793
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality

Insert Length: 384 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..61
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2049938"
/tissue_type="stem cell 34+/38+"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP HSC2"
/note="Organ: bone marrow; Vector: pAMP1; mRNA made from
bone marrow, stem cells 34+/38+, cDNA made by oligo-dT
priming. Directionally cloned. Size-selected on agarose
gel, average insert size 400 bp. Primary library,
non-amplified."

ORIGIN
Query Match 52.4%; Score 15.2; DB 9; Length 61;
Best Local Similarity 53.6%; Pred. No. 2e+05;
Matches 15; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUAAGCCCAAGGCC 28
Db 1 AAGGGTTCGTGCTGTATGACCTAAGGCC 28

RESULT 16
BM517546
LOCUS
DEFINITION Xj8007.y1 Ascaris suum female head SL1 TOPO v1 Murphy Chiapelli
McCartner Ascaris suum cDNA 5'; mRNA sequence.
ACCESSION BM517546
VERSION BM517546.1 GI:18688698
KEYWORDS EST.
SOURCE Ascaris suum (pig roundworm)
ORGANISM Ascaris suum
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
AUTHORS Ascaridoidea; Ascaridae; Ascaris.
1 (bases 1 to 65)
McCartner, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, I., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagarelashvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Persor, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCartner, J.P
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estwaterston.wustl.edu
The library was constructed by Claire Murphy, Brandi Chiapelli, and
Dr. James McCartner at Washington University, St. Louis. DNA
Sequencing by: Washington University Genome Sequencing Center.
Location/Qualifiers
1..65
source
/organism="Ascaris suum"
/mol_type="mRNA"
/db_xref="taxon:6253"
/sex="female"
/tissue_type="Head"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Ascaris suum female head SL1 TOPO v1 Murphy
Chiapelli McCartner"
/note="Vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI;


```

Site 2: EcoRI; The library was constructed by Claire Murphy, Brandi Chiapelli, and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-S1 PCR based library. Ascaris sum female head cDNA PCR products of size >400 nucleotides containing S11 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(invitrogen) following the TOPO TA cloning protocol. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@jhsph.edu) of the School of Public Hygiene and Public Health at John Hopkins University in Baltimore, MD"

ORIGIN

Query Match 52.4%; Score 15.2; DB 12; Length 65;
Best Local Similarity 42.9%; Pred. No. 2e+05;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 2 AAGAUCUUUUUUAAGCCCAAGGCGU 29

Db 1 AAGTTCTGTTTATGAGACCGAGATCT 28

RESULT 17

AA936218/c
LOCUS
DEFINITION
ON43C10.s1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1559442 3',
78 bp mRNA linear EST 23-JUN-1998
mRNA sequence.

ACCESSION
AA936218

VERSION
AA936218.1 GI:3094136

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Carchhini; Hominidae; Homo.

1 (bases 1 to 78)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgap@remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www-bio.lnl.gov/bbrp/image/image.html

Insert Length: 1346 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 52.

FEATURES

Location/Qualifiers

1..78

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1559442"

/tissue_type="adenocarcinoma"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_C08"

/note="Organ: colon; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Donaldo."

ORIGIN

Query Match 52.4%; Score 15.2; DB 9; Length 78;

Best Local Similarity 46.4%; Pred. No. 1.9e+05;

Matches 13; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 2 AAGAUCUUUUUUAAGCCCAAGGCGU 29

Db 77 AGTTCTGTTTATGAGACCGACCCCT 50

RESULT 18

B02943/c
LOCUS
DEFINITION
B02943 58 bp DNA linear GSS 13-JUL-1996
sapiens genomic clone cSRL-163G2, genomic survey sequence.

ACCESSION
B02943.1 GI:1412221

VERSION
GSS.

KEYWORDS
SOURCE

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 58)

Jones, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M.,

Harris, J., DeFord, J., McFarland, J., Burzinski, K., Khan, M.,

Kupfer, K. and Garner, H.R.

Genomic Sequence Sampled Map of Chromosome 11

Unpublished (1996)

Contact: Evans GA, Shane Probst

McDermott Center for Human Growth and Development

University of Texas Southwestern Medical Center At Dallas

5323 Harry Hines Blvd, Dallas TX 75235-8591

Tel: 214-648-1600

Fax: 214-648-1666

Email: gevan@utsw.swmed.edu, shane@mcdermott.swmed.edu

Seq primer: T7

Class: cosmid ends

High quality sequence stop: 58.

FEATURES

Location/Qualifiers

1..58

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="cSRL-163G2"

/sex="female"

/cell_type="chimeric hamster somatic cell hybrid"

/clone_lib="cSRL flow sorted Chromosome 11 specific

cosmid"

/note="Vector: sCos-1; Human Chromosome 11 specific cosmid

library prepared from flow sorted human Chromosome 11

derived from Chinese Hamster Ovary (CHO) monochromosomal

somatic cell hybrid, J1"

ORIGIN

Query Match 51.7%; Score 15; DB 28; Length 58;

Best Local Similarity 43.5%; Pred. No. 2.4e+05;

Matches 10; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 6 UCUUUUUUAAGCCCAAGGCGC 28

Db 41 TTTTCTTTTGTATCCCAAGGCGC 19

RESULT 19

CD682098/c
LOCUS
DEFINITION
rJ46C08.y1 Meloidogyne chitwoodi egg SL1 TOPO v1 Meloidogyne
chitwoodi cDNA 5', mRNA sequence.

ACCESSION
CD682098

VERSION
CD682098.1 GI:32183864

KEYWORDS
EST.

ORGANISM
Meloidogyne chitwoodi

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

TITLE Exon-trap tags from a T47D GenomeScreen(TM) Library
JOURNAL Unpublished (2000)
COMMENT Contact: Greg Henkel
Gene Expression

Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkel@aurorabio.com

Pools of cells were isolated from a GenomeScreen(TM) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase preceded by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAMP-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.

Class: exon-trapped.

FEATURES

source

1. .49
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Carcinoma"
/cell_type="Epithelial"
/cell_line="T47D"
/clone_lib="Genetrap T47D Human Breast Carcinoma Library"
/notes="Organ: Breast; Vector: pAMP-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAMP-1 and used to transform DH5-alpha competent bacteria."

ORIGIN

Query Match 51.0%; Score 14.8; DB 28; Length 49;
Best Local Similarity 57.7%; Pred. No. 3e+05;
Matches 15; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAAGAUUUUUUUUAGGCCCAAG 26
||||| : : : : :
Db 6 AAAGAGACTTCCTGTAGCGCAAG 31

RESULT 22

AI224478/c
LOCUS AI224478 55 bp mRNA linear EST 21-DEC-1998
DEFINITION qx0606.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2000555 3' similar to TR:023462 Q23462 HYPOTHETICAL 18.0 KD PROTEIN. ;, mRNA sequence.

ACCESSION AI224478.1 GI:3807191

VERSION AI224478

KEYWORDS EST.

SOURCE Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 55)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

unknown library type

Trace considered overall poor quality

Insert Length: 1214 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

source

1. .55
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:2000555"
/tissue_type="lymphoma, follicular mixed small and large cell"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

ORIGIN

Query Match 51.0%; Score 14.8; DB 9; Length 55;
Best Local Similarity 38.5%; Pred. No. 2.9e+05;
Matches 10; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 4 GAUUCUUUUUUAAGCCCAAGGCU 29
||| : : : : :
Db 30 GTTTTITTTTTTCCCAAGGGTT 5

RESULT 23

B636255

LOCUS B636255

DEFINITION

SMOVMCAQ08C02SK Onchocerca volvulus adult male cDNA

(SAW98MLW-OvAM) Onchocerca volvulus cDNA clone SMOVMCAQ08C02 5', mRNA sequence.

ACCESSION B636255

VERSION B636255.1 GI:9919366

KEYWORDS EST.

SOURCE Onchocerca volvulus

ORGANISM Onchocerca volvulus

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; 1 (bases 1 to 64)

AUTHORS Lizotte-Waniewski, M. and Williams, S.A.

TITLE Genes expressed in adult male stage of Onchocerca volvulus

JOURNAL Unpublished (1998)

COMMENT Contact: Steven A. Williams

Molecular Parasitology

Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA

Tel: 4135853826

Fax: 4135853786

Email: genome@smith.edu

Seq primer: pBluescript SK.

Location/Qualifiers

source

1. .64

/organism="Onchocerca volvulus"

/mol_type="mRNA"

/db_xref="taxon:6282"

/clone="SMOVMCAQ08C02"

/sex="male"

/dev_stage="adult"

/lab_host="XLI-Blue MRF"

/clone_lib="Onchocerca volvulus adult male cDNA (SAW98MLW-OvAM)"

/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Filarial nematode parasite of humans. Six adult male worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult male mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA

pol I. The library has 2 x 10E5 independent recombinants and the average insert size is ~1100bp. The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available from Dr. Steven A. Williams, email: genome@smith.edu."

from Dr. Steven A. Williams, email: genome@smith.edu."

from Dr. Steven A. Williams, email: genome@smith.edu."

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from Dr. Steven A. Williams, email: genome@smith.edu."

from Dr. Steven A. Williams, email: genome@smith.edu."

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from Dr. Steven A. Williams, email: genome@smith.edu."

from Dr. Steven A. Williams, email: genome@smith.edu."

from Dr. Steven A. Williams, email: genome@smith.edu."

from Dr. Steven A. Williams, email: genome@smith.edu."

```

QY 4 GAUUCUUUUUGUAGCCCAAGCGGU 29
DB 15 GATTCTCTCTGTAGCGCAATGCT 40

RESULT 24
CG588850 67 bp DNA linear GSS 02-OCT-2003
DEFINITION OS1240321 Mus musculus 129Sv/Ev Mus musculus genomic clone
ACCESSION CG588850
VERSION CG588850
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 67)
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtehorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmiBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
source
1..67
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/Ev"
/db_xref="taxon:10090"
/clone="OS1240321"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Ev"

ORIGIN
Query Match 51.0%; Score 14.8; DB 29; Length 67;
Best Local Similarity 44.4%; Pred. No. 2.8e+05;
Matches 12; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAGAUUCUUUUUGUAGCCCAAGGG 27
DB 2 AAGGATTTTITTTGGAGACNCGGG 28

RESULT 25
AL780467/c 70 bp mRNA linear EST 12-NOV-2003
LOCUS AL780467
DEFINITION AL780467 XGC-neurula Silurana tropicalis cDNA clone TNeu071b11 5',
mRNA sequence.
ACCESSION AL780467
VERSION AL780467.2 GI:38286361
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis
REFERENCE 1 (bases 1 to 70)
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
TITLE Crouning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)

JOURNAL Unpublished (2003)
COMMENT On Jun 25, 2002 this sequence version replaced gi:21566171.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from Sug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli DH10B
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TNeu071b11.picSP6
Sequencing primer: SP6.
FEATURES
source
1..70
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TNeu071b11"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/clone_lib="XGC-neurula"
/notes="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from Sug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."

ORIGIN
Query Match 51.0%; Score 14.8; DB 9; Length 70;
Best Local Similarity 46.2%; Pred. No. 2.8e+05;
Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 4 GAUUCUUUUUGUAGCCCAAGCGGU 29
DB 54 GACTTGTGTTTGTGGCCCGCCGCGCT 29

RESULT 26
BZ289798/c 76 bp DNA linear GSS 24-OCT-2002
LOCUS BZ289798
DEFINITION SALK_023201.36.50.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_023201.36.50.x, genomic
survey sequence.
ACCESSION BZ289798
VERSION BZ289798.1 GI:24332044
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 76)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,W., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
source
1..76

```

BX650715 52 bp DNA linear GSS 09-OCT-2003
Arabidopsis thaliana T-DNA flanking sequence GK-52A09-021661,
 genomic survey sequence.

Strizhov.N., Li, Y., Rosso.M., Viehoever.P., Dekker.K., Siedler,H.
and Weishaar,B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished

A new *Arabidopsis thaliana* T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 52)
Strizhov,N., Li,Y., Rosso,M. and Weissshaar,B.
Direct Submission
Submitted (06-OCT-2003) Weissshaar B., Max-Planck-Institut fuer

This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone T16124. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

```

/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-552A09-021661"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA insertions. The lines were examined for the presence of the T-DNA from the T-DNA insertion lines."

```

vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequences were processed for submission. T-DNA derived sequences were removed."

```

      50.3%;   Score 14.6;  DB 29;      Length 52;
      Similarity 51.7%;   Pred. No. 3.5e+05;
      15; Conservative      5; Mismatches 9; Indels 0; Gaps 0;
1 AAAGAUUCUUUUUUAAGCCCGCAGGGCU 29

```

AL940874 53 bp DNA linear GSS 24-OCT-2002
Arabidopsis thaliana T-DNA flanking sequence GK-252G08-014577,
genomic survey sequence. AL940874

Arabidopsis thaliana T-DNA flanking sequence GK-2523G08-014377,
genomic survey sequence.
AL940874
AL940874.1 GI:24397472

KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicaceae; Arabidopsis.
AUTHORS 1 Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Siedler, H. and Weisshaar, B.
TITLE A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
JOURNAL Unpublished
REFERENCE 2 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
AUTHORS A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
TITLE Unpublished
JOURNAL 3 (bases 1 to 53)
REFERENCE Strizhov, N., Rosso, M., Li, Y. and Weisshaar, B.
AUTHORS Direct Submission
TITLE Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
JOURNAL This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F7F22. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
COMMENT http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
source
1..53
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="Colombia 0"
/db_xref="taxon:3702"
/clone="GK-252G08-014577"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"
ORIGIN
Query Match 50.3%; Score 14.6; DB 29; Length 53;
Best Local Similarity 44.8%; Pred. No. 3.5e+05;
Matches 13; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
Qy 1 AAAGAUCUUUUUUAAGCCCAAGGCU 29
Db 16 ATAATACCTTATCTAAGCCCTACCCCT 44

RESULT 30
BE970792 59 bp mRNA linear EST 04-OCT-2000
LOCUS 601680150R1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3950172 3',
DEFINITION mRNA sequence.
ACCESSION BE970792
VERSION BE970792.1 GI:10583725
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 59)
TITLE NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM816 row: d column: 13
High quality sequence stop: 57.
FEATURES
source
1..59
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3950172"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 78"
/notes="Organ: pancreas; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccctcgcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCCGCGGACATG-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.2 Kb (range 0.5-4.0 Kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
ORIGIN
Query Match 50.3%; Score 14.6; DB 10; Length 59;
Best Local Similarity 47.6%; Pred. No. 3.4e+05;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
Qy 6 UUCUUUUUUAAGCCCAAGC 26
Db 3 TTTTITTTTGAACCCCGAGG 23

RESULT 31
BQ479345 61 bp mRNA linear EST 03-JUN-2002
LOCUS Ku33d12.y1 Strongyloides ratti PA female naive SL1 TOPO v1
DEFINITION Strongyloides ratti cDNA similar to contains Alu repetitive element;; mRNA sequence.
ACCESSION BQ479345
VERSION BQ479345.1 GI:21315312
KEYWORDS EST.
SOURCE Strongyloides ratti
ORGANISM Strongyloides ratti
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Panagrolaimoidea; Strongyloidea; Strongyloides.
AUTHORS 1 (bases 1 to 61)
McCarte, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagaris, V., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Stepien, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
TITLE Unpublished (1999)
JOURNAL Contact: McCarte JP
COMMENT The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter

at Washington University, St. Louis. Parasitic adult females were collected from naive animals and provided by Dr. Mark Viney of University of Bristol, Bristol, UK (Mark.Viney@bristol.ac.uk).
Seq primer: SL1 primer.

FEATURES

source

Location/Qualifiers

1..61

/organism="Strongyloides ratti"

/mol_type="mRNA"

/db_xref="taxon:34506"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Strongyloides ratti PA female naive SL1 TOPO v1"

/note="vector: PCR11-TOPO (Invitrogen); Site 1: EcoRI; Site 2: EcoRI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into PCR11-TOPO(Invitrogen) following the TOPO TA cloning protocol. Parasitic adult females were collected from naive animals and provided by Dr. Mark Viney of University of Bristol, Bristol, UK (Mark.Viney@bristol.ac.uk)."

ORIGIN

Query Match 50.3%; Score 14.6; DB 13; Length 61;
Best Local Similarity 47.6%; Pred. No. 3.4e+05;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAGAUUCUUUUUAAGCCGCC 22

Db 32 AAAATGTTTTTGTAAAGACC 12

RESULT 32

AL763793/c

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-040F11-015225, genomic survey sequence.

ACCESSION

AL763793

VERSION

AL763793.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

REFERENCE

AUTHORS

TITLE

A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (17-JUN-2002) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany. This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone M4E13. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

Location/Qualifiers

source

1..65

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

ORIGIN

Query Match 50.3%; Score 14.6; DB 29; Length 65;
Best Local Similarity 48.3%; Pred. No. 3.4e+05;
Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGAUUCUUUUUAAGCCGCCAAGGCU 29

Db 52 ATAAATCTTTAAGTAGGCTCTAAAGGCT 24

RESULT 33

BZ768797/c

LOCUS

DEFINITION

Arabidopsis thaliana genomic clone SALK_140745.49.75.n, genomic survey sequence.

ACCESSION

BZ768797

VERSION

BZ768797.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

REFERENCE

AUTHORS

TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

source

1..69

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone_lib="SALK_140745.49.75.n"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

```

Query Match      50.3%; Score 14.6; DB 28; Length 69;
Best Local Similarity 52.4%; Pred. No. 3.3e+05;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUUGUAGCCC 21
    |||||:::|:::|:::|:::|
Db 48 AAAGATTCAATTTTAAAGCAC 28

RESULT 34
BZ768791/c
LOCUS      70 bp      DNA      linear      GSS 13-MAR-2003
DEFINITION SALK_140737.29.55.x.Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_140737.29.55.x, genomic
            survey sequence.
ACCESSION  BZ768791
VERSION     BZ768791.1 GI:28942475
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE  1 (bases 1 to 70)
AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
FEATURES   Class: TDNA tagged.
            Location/Qualifiers
                source
                1..70
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /strain="Columbia 0"
                /db_xref="taxon:3702"
                /clone="SALK_140737.29.55.x"
                /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                /note="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      50.3%; Score 14.6; DB 28; Length 70;
Best Local Similarity 52.4%; Pred. No. 3.3e+05;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUUGUAGCCC 21
    |||||:::|:::|:::|:::|
Db 49 AAAGATTCAATTTTAAAGCAC 29

RESULT 35
BZ768795/c
LOCUS      70 bp      DNA      linear      GSS 13-MAR-2003
DEFINITION SALK_140742.35.20.x.Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_140742.35.20.x, genomic
            survey sequence.
ACCESSION  BZ768795
VERSION     BZ768795.1 GI:28942479
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE  1 (bases 1 to 70)
AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
FEATURES   Class: TDNA tagged.
            Location/Qualifiers
                source
                1..70
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /strain="Columbia 0"
                /db_xref="taxon:3702"
                /clone="SALK_140737.29.55.x"
                /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                /note="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      50.3%; Score 14.6; DB 28; Length 70;
Best Local Similarity 52.4%; Pred. No. 3.3e+05;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUUGUAGCCC 21
    |||||:::|:::|:::|:::|
Db 49 AAAGATTCAATTTTAAAGCAC 29

RESULT 36
BZ768795/c
LOCUS      71 bp      mRNA      linear      EST 10-FEB-2003
DEFINITION tR35C09 Bos taurus Rumen #1 library Bos taurus cDNA, mRNA
            sequence.
ACCESSION  CB227161
VERSION     CB227161.1 GI:28297675
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
            1 (bases 1 to 71)
            Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Senses,C.W.,
            Gordon,P.M.K. and Moore,S.S.
            Gene Expression Profiling of the Bovine Gastrointestinal Tract
            Unpublished (2002)
            Contact: Dr. Stephen Moore
            Beef Genomics Laboratory
            Dept of AFNS, University of Alberta
            410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
            Tel: 780 492 0169
            Fax: 780 492 4265

```

```

VERSION  BZ768795.1 GI:28942479
KEYWORDS GSS.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 70)
AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
FEATURES   Class: TDNA tagged.
            Location/Qualifiers
                source
                1..70
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /strain="Columbia 0"
                /db_xref="taxon:3702"
                /clone="SALK_140742.35.20.x"
                /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                /note="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      50.3%; Score 14.6; DB 28; Length 70;
Best Local Similarity 52.4%; Pred. No. 3.3e+05;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUUGUAGCCC 21
    |||||:::|:::|:::|:::|
Db 49 AAAGATTCAATTTTAAAGCAC 29

RESULT 36
BZ768795/c
LOCUS      71 bp      mRNA      linear      EST 10-FEB-2003
DEFINITION tR35C09 Bos taurus Rumen #1 library Bos taurus cDNA, mRNA
            sequence.
ACCESSION  CB227161
VERSION     CB227161.1 GI:28297675
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
            1 (bases 1 to 71)
            Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Senses,C.W.,
            Gordon,P.M.K. and Moore,S.S.
            Gene Expression Profiling of the Bovine Gastrointestinal Tract
            Unpublished (2002)
            Contact: Dr. Stephen Moore
            Beef Genomics Laboratory
            Dept of AFNS, University of Alberta
            410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
            Tel: 780 492 0169
            Fax: 780 492 4265

```

Email: stephen.moore@ualberta.ca
Insert Length: 71 Std Error: 0.00
POLYA-Yes

FEATURES

source

Location/Qualifiers

```
1. .71
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Smooth muscle"
/cell_type="Stratified squamous epithelial"
/dev_stage="Young adult"
/lab_host="XLI-BlueMRF strain"
/clone_lib="Bos taurus Rumex #1 library"
/notes="Organ: Rumex; Vector: Uni-2ZAPXR; Site_1: EcoRI;
Site_2: Xho I"
```

ORIGIN

Query Match 50.3%; Score 14.6; DB 14; Length 71;
Best Local Similarity 47.6%; Pred. No. 3.3e+05;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy

6 UUUUUUUUUAAGCCCAAGG 26

Db

55 TTTTGTGGAGCTCCCAAGG 35

RESULT 37

AZ833202

LOCUS

2M0115E08F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0115E08 F, genomic survey sequence.

ACCESSION

AZ833202

VERSION

AZ833202.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 71)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunnogenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0115 row: E column: 08
Seq primer: CTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 71.
Location/Qualifiers

FEATURES

source

```
1. .71
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0115E08"
/sex="Male"
/lab_host="E. Coli strain XLI0-Gold, T1-resistant, F-"  
/clone_lib="Mouse 10kb plasmid UUC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA
```

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XLI0-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 50.3%; Score 14.6; DB 28; Length 71;
Best Local Similarity 41.4%; Pred. No. 3.3e+05;
Matches 12; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy

1 AAAGAUUUUUUUAAGCCCAAGGCU 29

Db

23 AAAGATTCCTTCTCAACTGCTAAATGTT 51

RESULT 38

AI696772

LOCUS

wc61d07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323117 3',
mRNA sequence.

ACCESSION

AI696772

VERSION

AI696772.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 75)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbdp/image/image.html
Insert Length: 1931 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 51.
Location/Qualifiers

FEATURES

source

```
1. .75
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2323117"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pan1"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.72 Kb. Life Technologies catalog #:  
11548-013"
```

ORIGIN

Query Match 50.3%; Score 14.6; DB 9; Length 75;
Best Local Similarity 51.7%; Pred. No. 3.3e+05;
Matches 15; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy

1 AAAGAUUUUUUUAAGCCCAAGGCU 29

```

Db      25 AATATAGTAGTGATACCAACCAAGGCT 53
      ||| : : : : ||| : ||| : ||| :
RESULT 39
AL770832      80 bp      DNA      linear      GSS 19-JUN-2002
LOCUS      Arabidopsis thaliana T-DNA flanking sequence GK-175B08-013532,
DEFINITION      genomic survey sequence.
ACCESSION      AL770832
VERSION      AL770832.1
KEYWORDS      GI:215333034
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE      1 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
            A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
            Unpublished
JOURNAL
REFERENCE      2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
            A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
            Unpublished
JOURNAL
REFERENCE      3 (bases 1 to 80)
            Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.
            Direct Submission
            Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
            This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone F21P8. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
            Location/Qualifiers
FEATURES      source
            1..80
               /organism="Arabidopsis thaliana"
               /mol_type="genomic DNA"
               /strain="Columbia 0"
               /db_xref="taxon:3702"
               /clone="GK-175B08-013532"
               /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
               /notes="PCR was performed on DNA from Arabidopsis thaliana
               plants (T1) which were transformed with the T-DNA from
               vector pAC161. The lines contain one or more T-DNA
               insertions. The DNA fragment(s) resulting from the PCR
               were directly sequenced to determine the genomic sequence
               flanking the insertion. Sequences displaying significant
               similarity to the A. thaliana nuclear genome sequences were
               processed for submission. T-DNA derived sequences were
               removed"
ORIGIN
Query Match      50.3%; Score 14.6; DB 29; Length 80;
Best Local Similarity 48.3%; Pred. No. 3.2e+05;
Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY      1 AAGAATUUCUUUUAAGCCCAAGGCU 29
      ||| : ||| : ||| : ||| :
Db      39 AATAGTCTTTTCACACCTATGGGAT 67
      ||| : ||| : ||| : ||| :

RESULT 40
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LOCUS      Arabidopsis thaliana T-DNA flanking sequence GK-708H02-022874,
DEFINITION      genomic survey sequence.
ACCESSION      BX662819
VERSION      BX662819.1
KEYWORDS      GI:37619241
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE      1 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
            A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
            Unpublished
JOURNAL
REFERENCE      2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
            A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
            Unpublished
JOURNAL
REFERENCE      3 (bases 1 to 80)
            Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.
            Direct Submission
            Submitted (06-OCT-2003) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
            This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone MM17. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
            Location/Qualifiers
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               /notes="PCR was performed on DNA from Arabidopsis thaliana
               plants (T1) which were transformed with the T-DNA from
               vector pAC161. The lines contain one or more T-DNA
               insertions. The DNA fragment(s) resulting from the PCR
               were directly sequenced to determine the genomic sequence
               flanking the insertion. Sequences displaying significant
               similarity to the A. thaliana nuclear genome sequences were
               processed for submission. T-DNA derived sequences were
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ORIGIN
Query Match      50.3%; Score 14.6; DB 29; Length 80;
Best Local Similarity 47.6%; Pred. No. 3.2e+05;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

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Db      27 TTTTGTATATCTCAAGGCT 47
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Search completed: April 18, 2004, 09:59:30
Job time : 1553.67 secs

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 08:41:44 ; Search time 159.667 Seconds
(without alignments)

812.711 Million cell updates/sec

Title: US-09-310-844C-25

Perfect score: 29

Sequence: 1 aaagaucuuuuuuaagcccaaggcu 29

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters: 1657369

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	15.2	52.4	47	15	US-10-349-143-1097
C 5	15.2	52.4	60	10	US-09-908-975-18725
C 6	15	51.7	39	14	US-10-116-519-18
C 7	15	51.7	60	10	US-09-908-975-12187
C 8	15	51.7	65	10	US-09-908-975-4580
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C 12	14.6	50.3	60	10	US-09-908-975-18114
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C 14	14.6	50.3	60	16	US-10-231-494-24
C 15	14.6	50.3	75	9	US-09-864-761-23841

C 16	14.4	49.7	31	10	US-09-848-754A-6937
C 17	14.4	49.7	31	10	US-09-740-332-5660
C 18	14.4	49.7	31	10	US-09-817-879-5660
C 19	14.4	49.7	65	10	US-09-908-975-3924
C 20	14.4	49.7	65	10	US-09-908-975-30555
C 21	14.2	49.0	25	9	US-09-827-998-1098
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ALIGNMENTS

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; Sequence 178864, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-09-28
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; PRIOR FILING DATE: 1999-08-09
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; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
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; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178864
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Best Local Similarity 59.3%; Pred. No. 2.5e+03;
Matches 16; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
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US-09-983-965-4754
; Sequence 4754, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Ningbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathaleagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
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; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
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US-09-983-965-4754

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Matches 11; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

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; Sequence 1097, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
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; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
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US-10-349-143-1097

Query Match      52.4%; Score 15.2; DB 15; Length 47;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
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RESULT 5
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; Sequence 18725, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Lia
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
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; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18725
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-18725

Query Match      52.4%; Score 15.2; DB 10; Length 60;
Best Local Similarity 60.0%; Pred. No. 4.6e+03;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 7 UCUUUUUGUAGCCCAAGG 26
   |||:||||:|||||
Db 26 TCTTCTGAAAGCCCATGG 7

RESULT 6
US-10-116-519-18
; Sequence 18, Application US/10116519
; Publication No. US20030114373A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL CYSTEINE PROTEASE OF THE CALPAIN
; FILE REFERENCE: D0124 NP
; CURRENT APPLICATION NUMBER: US/10/116,519
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/281,253
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/288,768
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/296,180
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/300,620
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-519-18

Query Match      51.7%; Score 15; DB 14; Length 39;
Best Local Similarity 56.5%; Pred. No. 5.1e+03;
Matches 13; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GAUUCUUUUUGUAGCCCAAGG 26
   |||:||||:|||||
Db 5 GGTTCCTTCTGAAAGCTCAAGG 27

RESULT 7
US-09-908-975-12187/c
; Sequence 12187, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Lia
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
```

```
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 12187
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-12187

Query Match      51.7%; Score 15; DB 10; Length 60;
Best Local Similarity 47.8%; Pred. No. 5.6e+03;
Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      3 AGAUUUUUUUUUUAAGCCCAAG 25
      |||:::|:::|:::|:::|
Db      55 AGATTCTTCTGTAGCCGCTAAG 33

RESULT 8
US-09-908-975-4580
; Sequence 4580, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4580
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-908-975-4580

Query Match      51.7%; Score 15; DB 10; Length 65;
Best Local Similarity 56.5%; Pred. No. 5.7e+03;
Matches 13; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGAUUUUUUUUAAGCCCAAA 24
      |||:::|:::|:::|:::|
Db      34 AAGATGCTTCTGTGAAGCAACA 56

RESULT 9
US-09-839-478-31/c
; Sequence 31, Application US/09839478
; Publication No. US20030180724A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Sprecher, Cynthia J.
; APPLICANT: Lins, Ann M.
; TITLE OF INVENTION: MULTIPLEX AMPLIFICATION OF SHORT TANDEM
; REPEAT LOCI
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: P. O. Box 2599
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/839,478
; FILING DATE: 20-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/316,544
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-839-478-31

Query Match      51.0%; Score 14.8; DB 10; Length 29;
Best Local Similarity 42.3%; Pred. No. 5.9e+03;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY      4 GAUUCUUUUUUAAGCCCAAGGGCU 29
      |||:::|:::|:::|:::|
Db      29 GATTATCTTTCATCCACTAGGGCT 4

RESULT 10
US-10-005-530-18
; Sequence 18, Application US/10005530
; Publication No. US20030026795A1
; GENERAL INFORMATION:
; APPLICANT: Isaac, Barbara G.
; APPLICANT: Greenplate, John T.
; APPLICANT: Purcell, John P.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING INSECTS
; FILE REFERENCE: 11899.0022.DVUS01 (MOBT:022--2)
; CURRENT APPLICATION NUMBER: US/10/005,530
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 09/063,733
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/044,504
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-005-530-18

Query Match      50.3%; Score 14.6; DB 14; Length 25;
Best Local Similarity 47.6%; Pred. No. 7.1e+03;
Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      2 AAGAUUUUUUUUAAGCCCC 22
      |||:::|:::|:::|:::|
Db      5 AAGCTTCCTTCTTGTAATACCC 25

RESULT 11
```

```
US-09-908-975-8435
; Sequence 8435, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36888-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8435
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-8435

Query Match 50.3%; Score 14.6; DB 10; Length 60;
Best Local Similarity 51.7%; Pred. No. 8.6e+03;
Matches 15; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAAGAUCUUUUUUAAGCCCAAGGCU 29
DB 12 AACGAACGTGATGTAATCCCGAGGATCT 40

RESULT 12
US-09-908-975-18114
; Sequence 18114, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36888-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18114
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-18114

Query Match 50.3%; Score 14.6; DB 10; Length 60;
Best Local Similarity 52.4%; Pred. No. 8.6e+03;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 9 UUUUUUAAGCCCAAGGCU 29
DB 7 TATTCTGAGTCCCAAGGCT 27

RESULT 13
US-10-378-094-45
; Sequence 45, Application US/10378094
; Publication No. US20030221201A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378,094
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide encoding peptide with EPO activity
US-10-378-094-45

Query Match 50.3%; Score 14.6; DB 15; Length 60;
Best Local Similarity 52.4%; Pred. No. 8.6e+03;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 UUCUUUUUAAGCCCAAGG 26
DB 36 TTGGTTTGTAGCCCAAGG 56

RESULT 14
US-10-231-494-24
; Sequence 24, Application US/10231494
; Publication No. US2004002334A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: sequences
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(60)
US-10-231-494-24

Query Match 50.3%; Score 14.6; DB 16; Length 60;
Best Local Similarity 52.4%; Pred. No. 8.6e+03;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 UUCUUUUUAAGCCCAAGG 26
DB 36 TTGGTTTGTAGCCCAAGG 56
```

RESULT 15

US-09-864-761-23841/c
; Sequence 23841, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23841
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC01111.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9
; OTHER INFORMATION: NT HIT: G14506086, EVALUAE 9.10e+00
; OTHER INFORMATION: EST_HUMAN HIT: BE542663.1, EVALUAE 5.60e-02
US-09-864-761-23841
Query Match 50.3%; Score 14.6; DB 9; Length 75;
Best Local Similarity 48.3%; Pred. No. 9e+03;
Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

RESULT 16

US-09-848-754A-6937/c
; Sequence 6937, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE REFERENCE: MRHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6937
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-6937
Query Match 49.7%; Score 14.4; DB 10; Length 31;
Best Local Similarity 58.3%; Pred. No. 9.2e+03;
Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

RESULT 17

US-09-740-332-5660/c
; Sequence 5660, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5660
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: DNazyme
US-09-740-332-5660
Query Match 49.7%; Score 14.4; DB 10; Length 31;
Best Local Similarity 58.3%; Pred. No. 9.2e+03;
Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

RESULT 18

US-09-817-879-5660/c
; Sequence 5660, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
US-09-817-879-5660/c
Query Match 49.7%; Score 14.4; DB 10; Length 31;
Best Local Similarity 58.3%; Pred. No. 9.2e+03;
Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: Hepatitis C Virus Infection
; CURRENT APPLICATION NUMBER: US/09/817,879
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5660
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: DNazyme
; US-09-817-879-5660

Query Match          49.7%; Score 14.4; DB 10; Length 31;
Best Local Similarity 58.3%; Pred. No. 9.2e+03;
Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUUUAAGCCCAAG 25
   ||||| : : : |||||
Db 27 AAGATCGTTGTAGTACGCCCAAG 4

RESULT 19
US-09-908-975-3924/c
; Sequence 3924, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: THAT POPULATE A TRANSCRIPTOME
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3924
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-09-908-975-3924

Query Match          49.7%; Score 14.4; DB 10; Length 65;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 12; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAGAUUUUUUUUAAGCCCAAG 24
   ||||| : : : |||||
Db 35 AGAGATTCCTTTGTGAAGCGTAA 12

RESULT 20
US-09-975-30555
; Sequence 30555, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
```

```
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: THAT POPULATE A TRANSCRIPTOME
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30555
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-908-975-30555

Query Match          49.7%; Score 14.4; DB 10; Length 65;
Best Local Similarity 54.2%; Pred. No. 1.1e+04;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 5 AUUCUUUUUUUAAGCCCAAGGC 28
   ||||| : : : |||||
Db 32 ATTCTGTGTGAAGCCCACTGC 55

RESULT 21
US-09-827-998-1098/c
; Sequence 1098, Application US/09827998
; Patent No. US2002010252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acemica Sequence Listing Engine
; SEQ ID NO 1098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-827-998-1098

Query Match          49.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUUUUAAGCCCAAG 25
   ||||| : : : |||||
Db 25 TCTTTTGTAGTCCCTAAG 7

RESULT 22
US-09-827-998-1099/c
; Sequence 1099, Application US/09827998
; Patent No. US2002010252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
```

; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1099
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1099

Query Match 49.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUUGUAGCCCAAG 25
Db 24 TCTTTTGTAGTCCCTAAG 6

RESULT 23
US-09-827-998-1100/c
; Sequence 1100, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1100

Query Match 49.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUUGUAGCCCAAG 25
Db 23 TCTTTTGTAGTCCCTAAG 5

RESULT 24
US-09-827-998-1101/c
; Sequence 1101, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1101
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1101

Query Match 49.0%; Score 14.2; DB 9; Length 25;

Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 7 UCUUUUUGUAGCCCAAG 25
Db 22 TCTTTTGTAGTCCCTAAG 4

RESULT 25
US-09-827-998-1102/c
; Sequence 1102, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1102
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1102

Query Match 49.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUUGUAGCCCAAG 25
Db 21 TCTTTTGTAGTCCCTAAG 3

RESULT 26
US-09-827-998-1103/c
; Sequence 1103, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1103

Query Match 49.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUUGUAGCCCAAG 25
Db 20 TCTTTTGTAGTCCCTAAG 2

RESULT 27

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US-09-827-998-1104/c
; Sequence 1104, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-1104

Query Match          49.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUUUAAGCCCAAG 25
Db 19 TCTTTTGTAGTCCCTAAG 1

RESULT 28
US-10-675-685-1098/c
; Sequence 1098, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1098

Query Match          49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUUUAAGCCCAAG 25
Db 25 TCTTTTGTAGTCCCTAAG 7

RESULT 29
US-10-675-685-1099/c
; Sequence 1099, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
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US-10-675-685-1100/c
; Sequence 1100, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1100

Query Match          49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUUUAAGCCCAAG 25
Db 23 TCTTTTGTAGTCCCTAAG 5

RESULT 31
US-10-675-685-1101/c
; Sequence 1101, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1101
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1101

Query Match      49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAGGCCCAAG 25
Db 22 TCTTTTGTAGTCCCTAAG 4

RESULT 32
US-10-675-685-1102/c
; Sequence 1102, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1102
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1102

Query Match      49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAGGCCCAAG 25
Db 21 TCTTTTGTAGTCCCTAAG 3

RESULT 33
US-10-675-685-1103/c
; Sequence 1103, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1103

Query Match      49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAGGCCCAAG 25

RESULT 34
US-10-675-685-1104/c
; Sequence 1104, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-1104

Query Match      49.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 7 UCUUUUGUAGGCCCAAG 25
Db 19 TCTTTTGTAGTCCCTAAG 1

RESULT 35
US-10-098-263B-76444
; Sequence 76444, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 76444
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-76444

Query Match      49.0%; Score 14.2; DB 14; Length 25;
Best Local Similarity 47.4%; Pred. No. 1.1e+04;
Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 4 GAUUCUUUGUAGGCCCC 22
Db 1 GATACCTTTTAAATGCC 19

RESULT 36
US-10-287-919-545
; Sequence 545, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
```



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; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 545
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (143613)...(143638)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 638
US-10-287-919-545

Query Match          49.0%; Score 14.2; DB 14; Length 26;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 11 UUUUAAGCCCAAGGCGU 29
Db 2 TTTAGAGCCCAAGGCGT 20

RESULT 37
US-09-848-754A-6794/c
; Sequence 6794, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6794
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid

US-09-848-754A-6794

Query Match          49.0%; Score 14.2; DB 10; Length 31;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 AAGAUUCUUUUGUAGCCCAAGGCG 28
Db 27 AAGTCGTTGTAGCTAGCCCAAGGCG 1

RESULT 38
US-09-740-332-7606/c
; Sequence 7606, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7606
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: DNazyme

US-09-740-332-7606

Query Match          49.0%; Score 14.2; DB 10; Length 31;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAAGAUUCUUUUGUAGCCCAAGGG 27
Db 28 AAAGATCGTTGTAGCTAGCTCCAGGG 2

RESULT 39
US-09-817-879-7606/c
; Sequence 7606, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7606
; LENGTH: 31
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: DNazyme

US-09-817-879-7606

Query Match          49.0%; Score 14.2; DB 10; Length 31;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAAGAUUCUUUUGUAGCCCAAGGG 27
Db 28 AAAGATCGTTGTAGCTAGCTCCAGGG 2

RESULT 40
US-09-927-046-4415/c
; Sequence 4415, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channels
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4415
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-927-046-4415

Query Match          49.0%; Score 14.2; DB 12; Length 31;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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Tue Apr 20 10:03:05 2004

Qy 2 AAGAUUUUUUUUAAGCCCCAAGGC 28
Db 27 AATATCGTTGTAGCTAGCCCCCTAGGC 1

Search completed: April 18, 2004, 11:55:33
Job time : 166.667 secs

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 05:09:18 ; Search time 746.333 Seconds
(without alignments)
1684.164 Million cell updates/sec

Title: US-09-310-844C-24

Perfect score: 29

Sequence: 1 uauaauuuuuuuuagccuaggggcu 29

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1774092

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hsg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	29	100.0	42	6	BD274275	BD274275 Identific
2	29	100.0	42	6	BD274283	BD274283 Identific
3	28	96.6	46	6	BD274240	BD274240 Identific
4	28	96.6	46	6	BD274249	BD274249 Identific
5	28	96.6	46	6	BD274252	BD274252 Identific
6	28	96.6	46	6	BD274253	BD274253 Identific
7	28	96.6	46	6	BD274257	BD274257 Identific
8	28	96.6	46	6	BD274265	BD274265 Identific
9	28	96.6	46	6	BD274268	BD274268 Identific
10	28	96.6	46	6	BD274269	BD274269 Identific
11	25.8	89.0	42	6	BD274270	BD274270 Identific
12	25.8	89.0	42	6	BD274278	BD274278 Identific
13	24.8	85.5	46	6	BD274238	BD274238 Identific
14	24.8	85.5	46	6	BD274236	BD274236 Identific
15	23.8	82.1	42	6	BD274271	BD274271 Identific
16	23.8	82.1	42	6	BD274279	BD274279 Identific
17	23.8	82.1	46	6	BD274247	BD274247 Identific
18	23.8	82.1	46	6	BD274263	BD274263 Identific
19	23.2	80.0	42	6	BD274272	BD274272 Identific
20	23.2	80.0	42	6	BD274273	BD274273 Identific
21	23.2	80.0	42	6	BD274280	BD274280 Identific
22	23.2	80.0	42	6	BD274281	BD274281 Identific
23	22.6	77.9	42	6	BD274284	BD274284 Identific
24	22.2	76.6	46	6	BD274241	BD274241 Identific
25	22.2	76.6	46	6	BD274242	BD274242 Identific
26	22.2	76.6	46	6	BD274243	BD274243 Identific
27	22.2	76.6	46	6	BD274258	BD274258 Identific
28	22.2	76.6	46	6	BD274259	BD274259 Identific
29	22.2	76.6	46	6	BD274260	BD274260 Identific
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31	21.6	74.5	46	6	BD274248	BD274248 Identific
32	21.6	74.5	46	6	BD274262	BD274262 Identific
33	21.6	74.5	46	6	BD274264	BD274264 Identific
34	19.4	66.9	42	6	BD274276	BD274276 Identific
35	19.4	66.9	46	6	BD274237	BD274237 Identific
36	19.4	66.9	46	6	BD274251	BD274251 Identific
37	19.4	66.9	46	6	BD274255	BD274255 Identific
38	19.4	66.9	46	6	BD274257	BD274257 Identific
39	18.4	63.4	42	6	BD274274	BD274274 Identific
40	18.4	63.4	42	6	BD274282	BD274282 Identific
41	18	62.1	44	6	BD274277	BD274277 Identific
42	15.8	54.5	30	6	AX792238	AX792238 Sequence
43	15.4	53.1	41	6	AX514720	AX514720 Sequence
44	15.4	53.1	41	6	AX520728	AX520728 Sequence
45	15.2	52.4	33	6	AR020509	AR020509 Sequence
46	15	51.7	40	6	E49126	E49126 Novel G pro
47	15	51.7	40	6	E50836	E50836 Novel G pro
48	14.8	51.0	35	6	I08597	I08597 Sequence 12
49	14.8	51.0	35	6	AR364722	AR364722 Sequence
50	14.8	51.0	36	6	AR142180	AR142180 Sequence
51	14.8	51.0	43	6	AX483394	AX483394 Sequence
52	14.6	50.3	51	6	AX115517	AX115517 Sequence
53	14.6	50.3	51	10	AF328713	AF328713 Mus muscu
54	14.6	50.3	63	9	S63972	S63972 IGH (CDR3 r
55	14.6	50.3	65	6	AX484927	AX484927 Sequence
56	14.6	50.3	72	1	ECOPK102	M30729 E.coli/151
57	14.4	49.7	25	6	AX042583	AX042583 Sequence
58	14.4	49.7	25	6	AX043280	AX043280 Sequence
59	14.2	49.0	25	6	AR434675	AR434675 Sequence
60	14.2	49.0	25	6	AR434676	AR434676 Sequence
61	14.2	49.0	25	6	AR434677	AR434677 Sequence
62	14.2	49.0	25	6	AR434678	AR434678 Sequence
63	14.2	49.0	25	6	AR434679	AR434679 Sequence
64	14.2	49.0	25	6	AR434680	AR434680 Sequence
65	14.2	49.0	25	6	AR434681	AR434681 Sequence

C 66	14.2	49.0	35	6	AX298174 Sequence	AX298174 Sequence	139	13.4	46.2	41	6	AR171328
C 67	14.2	49.0	42	6	BD274272	BD274272 Identific	140	13.4	46.2	42	6	A70932
C 68	14.2	49.0	42	6	BD274273	BD274273 Identific	141	13.4	46.2	42	6	BD003417
C 69	14.2	49.0	42	6	BD274280	BD274280 Identific	142	13.4	46.2	43	8	ATH553793
C 70	14.2	49.0	42	6	BD274281	BD274281 Identific	143	13.4	46.2	47	6	AX194666
C 71	14.2	49.0	45	6	I04390	I04390 Sequence 25	C 144	13.4	46.2	47	6	AX378367
C 72	14.2	49.0	45	6	AX923415	AX923415 Sequence	145	13.4	46.2	49	3	DD063607
C 73	14.2	49.0	50	6	AX781523	AX781523 Sequence	C 146	13.4	46.2	51	6	E28219
C 74	14.2	49.0	51	6	AX817032	AX817032 Sequence	C 147	13.4	46.2	51	6	I26179
C 75	14.2	49.0	56	6	AX247478	AX247478 Sequence	148	13.4	46.2	52	6	BD270556
C 76	14.2	49.0	30	6	AR256904	AR256904 Sequence	149	13.4	46.2	52	6	AR208953
C 77	14.2	49.0	30	6	AR256906	AR256906 Sequence	150	13.4	46.2	52	6	AR228346
C 78	14.2	49.0	30	6	AX113961	AX113961 Sequence	151	13.4	46.2	52	6	AX046943
C 79	14.2	49.0	30	6	AX113963	AX113963 Sequence	152	13.4	46.2	52	6	AX428345
C 80	14.2	49.0	37	6	AR003420	AR003420 Sequence	153	13.4	46.2	52	6	BD082716
C 81	14.2	49.0	37	6	I21209	I21209 Sequence 55	C 154	13.4	46.2	54	6	AX404651
C 82	14.2	49.0	37	6	I74476	I74476 Sequence 55	C 155	13.4	46.2	56	6	AX523133
C 83	14.2	49.0	37	6	AX555864	AX555864 Sequence	156	13.4	46.2	57	8	AX591789
C 84	14.2	49.0	37	6	AX555865	AX555865 Sequence	C 157	13.4	46.2	60	6	AR254137
C 85	14.2	49.0	44	6	AR003419	AR003419 Sequence	C 158	13.4	46.2	60	8	AX596988
C 86	14.2	49.0	44	6	I21208	I21208 Sequence 54	C 159	13.4	46.2	61	14	ALRBSSE16
C 87	14.2	49.0	44	6	I74475	I74475 Sequence 54	C 160	13.4	46.2	65	6	AX484878
C 88	14.2	49.0	55	8	AX598912	AX598912 Arabidops	161	13.4	46.2	77	8	SPO222770
C 89	14.2	49.0	60	6	AX676039	AX676039 Sequence	C 162	13.2	45.5	25	6	AR434674
C 90	14.2	49.0	62	6	AX899399	AX899399 Sequence	163	13.2	45.5	26	8	ATH529956
C 91	14.2	49.0	62	6	BD034932	BD034932 Sequence	164	13.2	45.5	27	6	BD230947
C 92	14.2	49.0	78	14	AF362846	AF362846 HIV-1 iso	165	13.2	45.5	27	6	BD231661
C 93	14.2	49.0	78	14	AF362847	AF362847 HIV-1 iso	166	13.2	45.5	27	6	BD233712
C 94	14.2	49.0	78	14	AF362849	AF362849 HIV-1 iso	167	13.2	45.5	27	6	BD243600
C 95	13.8	47.6	17	6	AR433860	AR433860 Sequence	168	13.2	45.5	27	6	BD243606
C 96	13.8	47.6	25	6	AR434682	AR434682 Sequence	169	13.2	45.5	27	6	BD248833
C 97	13.8	47.6	25	6	AR434683	AR434683 Sequence	170	13.2	45.5	27	6	BD249071
C 98	13.8	47.6	25	6	AX527257	AX527257 Sequence	171	13.2	45.5	27	6	BD249129
C 99	13.8	47.6	31	6	AX426018	AX426018 Sequence	172	13.2	45.5	27	6	BD249183
C 100	13.8	47.6	36	6	AR142182	AR142182 Sequence	173	13.2	45.5	27	6	BD249801
C 101	13.8	47.6	42	6	AX017119	AX017119 Sequence	174	13.2	45.5	27	6	BD249894
C 102	13.8	47.6	42	6	AX017120	AX017120 Sequence	175	13.2	45.5	27	6	BD249953
C 103	13.8	47.6	42	6	AX017120	AX017120 Sequence	176	13.2	45.5	27	6	BD250041
C 104	13.8	47.6	50	6	AR288904	AR288904 Sequence	177	13.2	45.5	27	6	BD250098
C 105	13.8	47.6	50	6	AX157596	AX157596 Sequence	178	13.2	45.5	27	6	BD250169
C 106	13.8	47.6	50	6	AX164887	AX164887 Sequence	179	13.2	45.5	27	6	BD250169
C 107	13.8	47.6	59	10	CRUDELFNF	M27128 Chinese Ham	180	13.2	45.5	27	6	BD252043
C 108	13.8	47.6	65	6	AX482858	AX482858 Sequence	181	13.2	45.5	27	6	BD260155
C 109	13.8	47.6	79	6	AX914035	AX914035 Sequence	182	13.2	45.5	27	6	BD260603
C 110	13.8	47.6	79	6	BD049568	BD049568 Sequence	183	13.2	45.5	27	6	BD260661
C 111	13.6	46.9	25	6	AX610026	AX610026 Sequence	184	13.2	45.5	27	6	BD260720
C 112	13.6	46.9	25	6	AX610027	AX610027 Sequence	185	13.2	45.5	27	6	BD260786
C 113	13.6	46.9	31	6	AX223502	AX223502 Sequence	186	13.2	45.5	27	6	BD260940
C 114	13.6	46.9	31	6	AX249149	AX249149 Sequence	187	13.2	45.5	27	6	BD260946
C 115	13.6	46.9	37	6	AX183756	AX183756 Sequence	188	13.2	45.5	27	6	BD264592
C 116	13.6	46.9	40	6	AX456426	AX456426 Sequence	189	13.2	45.5	27	6	BD266680
C 117	13.6	46.9	42	6	AR264216	AR264216 Sequence	190	13.2	45.5	27	6	BD266910
C 118	13.6	46.9	44	6	A36495	A36495 Sequence 36	191	13.2	45.5	27	6	BD266916
C 119	13.6	46.9	44	6	AR080128	AR080128 Sequence	192	13.2	45.5	27	6	BD269268
C 120	13.6	46.9	47	6	AR290551	AR290551 Sequence	193	13.2	45.5	27	6	BD269733
C 121	13.6	46.9	50	6	AX160546	AX160546 Sequence	194	13.2	45.5	27	6	BD270314
C 122	13.6	46.9	51	6	AX160545	AX160545 Sequence	195	13.2	45.5	27	6	BD270314
C 123	13.6	46.9	51	6	AX160547	AX160547 Sequence	196	13.2	45.5	27	6	BD271538
C 124	13.6	46.9	51	6	AX498444	AX498444 Sequence	197	13.2	45.5	27	6	BD275003
C 125	13.6	46.9	55	6	AR358906	AR358906 Sequence	198	13.2	45.5	27	6	BD275062
C 126	13.6	46.9	68	1	AF178N01S1	AF178N01 Chlamydia	199	13.2	45.5	27	6	BD275124
C 127	13.6	46.9	68	1	LAWREN10	K03314 Bacterioph	200	13.2	45.5	27	6	BD275181
C 128	13.4	46.2	25	6	AX043007	AX043007 Sequence	201	13.2	45.5	27	6	BD275270
C 129	13.4	46.2	26	6	BD238414	BD238414 Sorting O	202	13.2	45.5	27	6	BD275327
C 130	13.4	46.2	26	6	AX431395	AX431395 Sequence	203	13.2	45.5	27	6	BD275386
C 131	13.4	46.2	26	6	AX055927	AX055927 Sequence	204	13.2	45.5	27	6	BD275445
C 132	13.4	46.2	26	6	BD190535	BD190535 Method fo	205	13.2	45.5	27	6	BD275501
C 133	13.4	46.2	30	6	AX790896	AX790896 Sequence	206	13.2	45.5	27	6	BD275925
C 134	13.4	46.2	31	6	AX426127	AX426127 Sequence	207	13.2	45.5	27	6	BD276018
C 135	13.4	46.2	35	6	AX367005	AX367005 Sequence	208	13.2	45.5	27	6	BD276331
C 136	13.4	46.2	38	6	BD170439	BD170439 Transgeni	209	13.2	45.5	27	6	AR184060
C 137	13.4	46.2	41	6	AR049546	AR049546 Sequence	210	13.2	45.5	27	6	AR203345
C 138	13.4	46.2	41	6	AR065751	AR065751 Sequence	211	13.2	45.5	27	6	AR206967

C 358	12.8	44.1	30	6	AX791737	AX791737 Sequence	C 431	12.6	43.4	29	6	I76812	I76812 Sequence 22
C 359	12.8	44.1	30	6	AX793354	AX793354 Sequence	C 432	12.6	43.4	30	6	AR261297	AR261297 Sequence
C 360	12.8	44.1	31	6	AX221037	AX221037 Sequence	C 433	12.6	43.4	30	6	AX683638	AX683638 Sequence
C 361	12.8	44.1	31	6	AX426065	AX426065 Sequence	C 434	12.6	43.4	32	6	AR061867	AR061867 Sequence
C 362	12.8	44.1	35	11	C75690	C75690 Homo sapien	C 435	12.6	43.4	32	6	BD233998	BD233998 Multiple
C 363	12.8	44.1	38	6	AR048354	AR048354 Sequence	C 436	12.6	43.4	32	6	AR252858	AR252858 Sequence
C 364	12.8	44.1	38	6	I53406	I53406 Sequence 11	C 437	12.6	43.4	34	6	AR381466	AR381466 Sequence
C 365	12.8	44.1	39	6	A26290	A26290 Subtilisin	C 438	12.6	43.4	34	6	AR381469	AR381469 Sequence
C 366	12.8	44.1	39	6	A26922	A26922 oligonucleo	C 439	12.6	43.4	35	6	AX020426	AX020426 Sequence
C 367	12.8	44.1	39	6	I43379	I43379 Sequence 8	C 440	12.6	43.4	36	6	I57363	I57363 Sequence 6
C 368	12.8	44.1	40	6	AR079795	AR079795 Sequence	C 441	12.6	43.4	36	9	AF505540	AF505540 Homo sapi
C 369	12.8	44.1	40	6	AR081325	AR081325 Sequence	C 442	12.6	43.4	37	8	ATH552409	ATH552409 Arabidops
C 370	12.8	44.1	40	6	AR170685	AR170685 Sequence	C 443	12.6	43.4	40	6	AX774088	AX774088 Sequence
C 371	12.8	44.1	42	6	I86960	I86960 Sequence 49	C 444	12.6	43.4	41	6	AX519811	AX519811 Sequence
C 372	12.8	44.1	45	6	AR032518	AR032518 Sequence	C 445	12.6	43.4	42	6	BD274270	BD274270 Identific
C 373	12.8	44.1	45	6	AR0332730	AR0332730 Sequence	C 446	12.6	43.4	42	6	BD274278	BD274278 Identific
C 374	12.8	44.1	45	6	I29258	I29258 Sequence 13	C 447	12.6	43.4	43	6	AS0152	AS0152 Sequence 9
C 375	12.8	44.1	45	6	I29470	I29470 Sequence 34	C 448	12.6	43.4	44	6	BD274261	BD274261 Identific
C 376	12.8	44.1	45	6	I90932	I90932 Sequence 13	C 449	12.6	43.4	45	6	AS1851	AS1851 Sequence 15
C 377	12.8	44.1	45	6	I31144	I31144 Sequence 34	C 450	12.6	43.4	45	6	AR085824	AR085824 Sequence
C 378	12.8	44.1	45	6	AR209182	AR209182 Sequence	C 451	12.6	43.4	45	6	AX554059	AX554059 Sequence
C 379	12.8	44.1	45	6	AR209394	AR209394 Sequence	C 452	12.6	43.4	46	6	BD274245	BD274245 Identific
C 380	12.8	44.1	47	6	AR288951	AR288951 Sequence	C 453	12.6	43.4	47	6	AR288361	AR288361 Sequence
C 381	12.8	44.1	47	6	AR289362	AR289362 Sequence	C 454	12.6	43.4	50	6	AX164808	AX164808 Sequence
C 382	12.8	44.1	48	14	SV4MNKVL	K00807 simian viru	C 455	12.6	43.4	50	6	AX164809	AX164809 Sequence
C 383	12.8	44.1	50	6	AR032731	AR032731 Sequence	C 456	12.6	43.4	51	6	AX157595	AX157595 Sequence
C 384	12.8	44.1	50	6	I29471	I29471 Sequence 34	C 457	12.6	43.4	51	6	AX190034	AX190034 Sequence
C 385	12.8	44.1	50	6	I91145	I91145 Sequence 34	C 458	12.6	43.4	51	6	AX190035	AX190035 Sequence
C 386	12.8	44.1	54	6	AR209395	AR209395 Sequence	C 459	12.6	43.4	55	6	AR238787	AR238787 Sequence
C 387	12.8	44.1	54	6	AR098551	AR098551 Sequence	C 460	12.6	43.4	55	6	AR079194	AR079194 Sequence
C 388	12.8	44.1	54	6	AR108893	AR108893 Sequence	C 461	12.6	43.4	55	6	S65927	S65927 immunoglob
C 389	12.8	44.1	54	6	AR268150	AR268150 Sequence	C 462	12.6	43.4	59	6	AX601370	AX601370 Sequence
C 390	12.8	44.1	54	6	AX009660	AX009660 Sequence	C 463	12.6	43.4	59	11	BX295121	BX295121 Arabidops
C 391	12.8	44.1	54	6	AX010922	AX010922 Sequence	C 464	12.6	43.4	61	8	AR241984	AR241984 Sequence
C 392	12.8	44.1	57	9	AF011598	AF011598 Homo sapi	C 465	12.6	43.4	61	8	AJ587776	AJ587776 Arabidops
C 393	12.8	44.1	58	6	I05513	I05513 Sequence 1	C 466	12.6	43.4	64	6	AR009650	AR009650 Sequence
C 394	12.8	44.1	58	6	I09141	I09141 Sequence 1	C 467	12.6	43.4	65	6	AX483070	AX483070 Sequence
C 395	12.8	44.1	59	8	AJ590671	AJ590671 Arabidops	C 468	12.6	43.4	65	6	AX484865	AX484865 Sequence
C 396	12.8	44.1	59	8	AJ599452	AJ599452 Arabidops	C 469	12.6	43.4	66	10	AF265740	AF265740 Mus muscu
C 397	12.8	44.1	63	6	I07555	I07555 Sequence 5	C 470	12.6	43.4	72	6	E01872	E01872 DNA encodin
C 398	12.8	44.1	65	6	AX482799	AX482799 Sequence	C 471	12.6	43.4	74	6	AX701724	AX701724 Sequence
C 399	12.8	44.1	65	6	AX483243	AX483243 Sequence	C 472	12.6	43.4	74	6	HUMAPOAG	M64418 Human apoli
C 400	12.8	44.1	65	6	AX483283	AX483283 Sequence	C 473	12.6	43.4	78	9	ATH527607	AJ527607 Arabidops
C 401	12.8	44.1	65	6	AX483721	AX483721 Sequence	C 474	12.6	43.4	79	14	MOKL	D13766 Mokola viru
C 402	12.8	44.1	65	6	AX483891	AX483891 Sequence	C 475	12.6	43.4	80	6	AS1846	AS1846 Sequence 10
C 403	12.8	44.1	65	6	AX484810	AX484810 Sequence	C 476	12.6	43.4	80	6	AS1883	AS1883 Sequence 47
C 404	12.8	44.1	66	8	AJ600346	AJ600346 Arabidops	C 477	12.6	43.4	80	6	BD208934	BD208934 Enzymatic
C 405	12.8	44.1	67	8	AF136104	AF136104 Ditrichum	C 478	12.6	43.4	80	11	BX294558	BX294558 Arabidops
C 406	12.8	44.1	68	6	AR356844	AR356844 Sequence	C 479	12.6	43.4	80	6	AR085848	AR085848 Sequence
C 407	12.8	44.1	68	6	AX908830	AX908830 Sequence	C 480	12.4	42.8	15	6	BD208934	BD208934 Enzymatic
C 408	12.8	44.1	68	6	BD044363	BD044363 Sequence	C 481	12.4	42.8	21	6	AR207325	AR207325 Sequence
C 409	12.8	44.1	69	6	AX904939	AX904939 Sequence	C 482	12.4	42.8	21	6	AR253153	AR253153 Sequence
C 410	12.8	44.1	69	6	BD040472	BD040472 Sequence	C 483	12.4	42.8	22	6	AR403671	AR403671 Sequence
C 411	12.8	44.1	69	14	AF092639	AF092639 HIV-1 pat	C 484	12.4	42.8	24	6	AR125043	AR125043 Sequence
C 412	12.8	44.1	75	8	ATH527247	ATH527247 Arabidops	C 485	12.4	42.8	25	6	AL16721	AL16721 oligonucleo
C 413	12.8	44.1	77	6	A38260	A38260 Sequence 15	C 486	12.4	42.8	25	6	AR134911	AR134911 Sequence
C 414	12.8	44.1	77	6	A38688	A38688 Sequence 15	C 487	12.4	42.8	25	6	AX042702	AX042702 Sequence
C 415	12.8	44.1	77	6	AR101813	AR101813 Sequence	C 488	12.4	42.8	25	6	AX042733	AX042733 Sequence
C 416	12.8	44.1	79	6	AR155054	AR155054 Sequence	C 489	12.4	42.8	25	6	AX042970	AX042970 Sequence
C 417	12.8	44.1	79	8	AR156303	AR156303 Sequence	C 490	12.4	42.8	25	6	AX043051	AX043051 Sequence
C 418	12.8	44.1	79	8	OSA532510	AJ532510 Oryza sat	C 491	12.4	42.8	25	6	AX043512	AX043512 Sequence
C 419	12.8	44.1	80	8	AJ593415	AJ593415 Arabidops	C 492	12.4	42.8	25	6	AX043553	AX043553 Sequence
C 420	12.8	44.1	80	8	AJ76928	AX476928 Sequence	C 493	12.4	42.8	25	6	AX527259	AX527259 Sequence
C 421	12.6	43.4	21	6	AX526304	AX526304 Sequence	C 494	12.4	42.8	25	6	AX527260	AX527260 Sequence
C 422	12.6	43.4	21	6	AX444982	AX444982 Sequence	C 495	12.4	42.8	25	6	AR020755	AR020755 Sequence
C 423	12.6	43.4	26	6	E22835	E22835 Promoter se	C 496	12.4	42.8	26	6	AR020771	AR020771 Sequence
C 424	12.6	43.4	26	6	AX067180	AX067180 Sequence	C 497	12.4	42.8	26	6	BD250380	BD250380 Enzyme . 7
C 425	12.6	43.4	26	6	BD177543	BD177543 Method fo	C 498	12.4	42.8	26	6	I34036	I34036 Sequence 10
C 426	12.6	43.4	29	6	AR018900	AR018900 Sequence	C 499	12.4	42.8	26	6	I34052	I34052 Sequence 29
C 427	12.6	43.4	29	6	AR066528	AR066528 Sequence	C 500	12.4	42.8	26	6	AX038769	AX038769 Sequence
C 428	12.6	43.4	29	6	AR112066	AR112066 Sequence	C 501	12.4	42.8	26	6	AR230012	AR230012 Sequence
C 429	12.6	43.4	29	6	BD261033	BD261033 Microbal	C 502	12.4	42.8	27	6	AX134143	AX134143 Sequence
C 430	12.6	43.4	29	6	I72245	I72245 Sequence 22	C 503	12.4	42.8	27	6		

C 504	12.4	42.8	29	6	ARI172337	Sequence	ARI172337	Sequence	12.2	42.1	21	12	AB068906
C 505	12.4	42.8	29	6	AR361352	Sequence	AR361352	Sequence	12.2	42.1	22	6	AR219168
C 506	12.4	42.8	30	6	AX922573	Sequence	AX922573	Sequence	12.2	42.1	24	6	AR360644
C 507	12.4	42.8	30	6	AX922583	Sequence	AX922583	Sequence	12.2	42.1	24	6	AR360644
C 508	12.4	42.8	31	6	BD002783	Gene comp	BD002783	Gene comp	12.2	42.1	25	6	AR434673
C 509	12.4	42.8	31	6	BD002783	Gene comp	BD002783	Gene comp	12.2	42.1	25	6	AR434673
C 510	12.4	42.8	35	6	AX085606	Sequence	AX085606	Sequence	12.2	42.1	25	6	AX006972
C 511	12.4	42.8	36	6	BD266502	Sequence	BD266502	Sequence	12.2	42.1	25	6	AX006973
C 512	12.4	42.8	38	6	AR331044	Sequence	AR331044	Sequence	12.2	42.1	25	6	AX042620
C 513	12.4	42.8	38	6	AX222612	Sequence	AX222612	Sequence	12.2	42.1	25	6	AX042620
C 514	12.4	42.8	39	6	BD233875	Novel met	BD233875	Novel met	12.2	42.1	25	6	AX043677
C 515	12.4	42.8	39	6	AX025305	Sequence	AX025305	Sequence	12.2	42.1	25	6	BD217278
C 516	12.4	42.8	39	6	AX113466	Sequence	AX113466	Sequence	12.2	42.1	25	6	BD217278
C 517	12.4	42.8	39	6	AX113601	Sequence	AX113601	Sequence	12.2	42.1	25	6	BD217278
C 518	12.4	42.8	39	6	AX494309	Sequence	AX494309	Sequence	12.2	42.1	25	6	BD217278
C 519	12.4	42.8	39	6	AX494310	Sequence	AX494310	Sequence	12.2	42.1	25	6	BD217278
C 520	12.4	42.8	39	6	AX816268	Sequence	AX816268	Sequence	12.2	42.1	25	6	BD217278
C 521	12.4	42.8	40	6	AR211425	Sequence	AR211425	Sequence	12.2	42.1	25	6	BD217278
C 522	12.4	42.8	40	6	AX515979	Sequence	AX515979	Sequence	12.2	42.1	25	6	BD217278
C 523	12.4	42.8	41	6	AX516345	Sequence	AX516345	Sequence	12.2	42.1	25	6	BD217278
C 524	12.4	42.8	41	6	AX516847	Sequence	AX516847	Sequence	12.2	42.1	25	6	BD217278
C 525	12.4	42.8	41	6	AX519357	Sequence	AX519357	Sequence	12.2	42.1	25	6	BD217278
C 526	12.4	42.8	41	6	AX519890	Sequence	AX519890	Sequence	12.2	42.1	25	6	BD217278
C 527	12.4	42.8	41	6	AX520379	Sequence	AX520379	Sequence	12.2	42.1	25	6	BD217278
C 528	12.4	42.8	42	6	AR393525	Sequence	AR393525	Sequence	12.2	42.1	25	6	BD217278
C 529	12.4	42.8	42	6	AR393525	Sequence	AR393525	Sequence	12.2	42.1	25	6	BD217278
C 530	12.4	42.8	43	6	AX484388	Sequence	AX484388	Sequence	12.2	42.1	25	6	BD217278
C 531	12.4	42.8	43	6	AX484576	Sequence	AX484576	Sequence	12.2	42.1	25	6	BD217278
C 532	12.4	42.8	44	6	AX008706	Sequence	AX008706	Sequence	12.2	42.1	25	6	BD217278
C 533	12.4	42.8	45	6	AX008707	Sequence	AX008707	Sequence	12.2	42.1	25	6	BD217278
C 534	12.4	42.8	47	6	AR288680	Sequence	AR288680	Sequence	12.2	42.1	25	6	BD217278
C 535	12.4	42.8	47	6	AR288680	Sequence	AR288680	Sequence	12.2	42.1	25	6	BD217278
C 536	12.4	42.8	47	6	AR288680	Sequence	AR288680	Sequence	12.2	42.1	25	6	BD217278
C 537	12.4	42.8	47	6	AR288680	Sequence	AR288680	Sequence	12.2	42.1	25	6	BD217278
C 538	12.4	42.8	50	6	BD014219	Probe for	BD014219	Probe for	12.2	42.1	25	6	BD217278
C 539	12.4	42.8	51	6	AX115185	Sequence	AX115185	Sequence	12.2	42.1	25	6	BD217278
C 540	12.4	42.8	51	10	MUSTC8YBF	Sequence	M36458 Mouse T-cell	Sequence	12.2	42.1	25	6	BD217278
C 541	12.4	42.8	51	6	AX16720	oligonucleo	AX16720 oligonucleo	Sequence	12.2	42.1	25	6	BD217278
C 542	12.4	42.8	53	6	ATH524831	Arabidops	ATH524831 Arabidops	Sequence	12.2	42.1	25	6	BD217278
C 543	12.4	42.8	56	8	AX002818	Sequence	AX002818	Sequence	12.2	42.1	25	6	BD217278
C 544	12.4	42.8	60	6	AX443288	Sequence	AX443288	Sequence	12.2	42.1	25	6	BD217278
C 545	12.4	42.8	64	6	BD273287	Genetic m	BD273287 Genetic m	Sequence	12.2	42.1	25	6	BD217278
C 546	12.4	42.8	65	6	AX443299	Sequence	AX443299	Sequence	12.2	42.1	25	6	BD217278
C 547	12.4	42.8	65	6	AX443299	Sequence	AX443299	Sequence	12.2	42.1	25	6	BD217278
C 548	12.4	42.8	65	6	AX483074	Sequence	AX483074	Sequence	12.2	42.1	25	6	BD217278
C 549	12.4	42.8	65	6	AX483283	Sequence	AX483283	Sequence	12.2	42.1	25	6	BD217278
C 550	12.4	42.8	65	6	AX485424	Sequence	AX485424	Sequence	12.2	42.1	25	6	BD217278
C 551	12.4	42.8	65	6	AX486235	Sequence	AX486235	Sequence	12.2	42.1	25	6	BD217278
C 552	12.4	42.8	65	6	AX486235	Sequence	AX486235	Sequence	12.2	42.1	25	6	BD217278
C 553	12.4	42.8	65	9	S81524	Sequence	S81524 RCI-NADH de	Sequence	12.2	42.1	25	6	BD217278
C 554	12.4	42.8	66	8	AJ597062	Arabidops	AJ597062 Arabidops	Sequence	12.2	42.1	25	6	BD217278
C 555	12.4	42.8	70	6	AR012564	Sequence	AR012564	Sequence	12.2	42.1	25	6	BD217278
C 556	12.4	42.8	70	6	AR020392	Sequence	AR020392	Sequence	12.2	42.1	25	6	BD217278
C 557	12.4	42.8	70	6	AR109413	Sequence	AR109413	Sequence	12.2	42.1	25	6	BD217278
C 558	12.4	42.8	70	6	AR123764	Sequence	AR123764	Sequence	12.2	42.1	25	6	BD217278
C 559	12.4	42.8	70	6	182738	Sequence	182738	Sequence	12.2	42.1	25	6	BD217278
C 560	12.4	42.8	70	6	AR368604	Sequence	AR368604	Sequence	12.2	42.1	25	6	BD217278
C 561	12.4	42.8	70	6	AR391796	Sequence	AR391796	Sequence	12.2	42.1	25	6	BD217278
C 562	12.4	42.8	72	6	109533	Sequence	109533	Sequence	12.2	42.1	25	6	BD217278
C 563	12.4	42.8	72	6	AX989785	Sequence	AX989785	Sequence	12.2	42.1	25	6	BD217278
C 564	12.4	42.8	72	6	BD034318	Sequence	BD034318	Sequence	12.2	42.1	25	6	BD217278
C 565	12.4	42.8	77	8	AX593524	Sequence	AX593524	Sequence	12.2	42.1	25	6	BD217278
C 566	12.4	42.8	78	14	S60076	anti	S60076 anti	Sequence	12.2	42.1	25	6	BD217278
C 567	12.4	42.8	78	14	AF362848	Sequence	AF362848	Sequence	12.2	42.1	25	6	BD217278
C 568	12.4	42.8	80	6	A52215	Sequence	A52215	Sequence	12.2	42.1	25	6	BD217278
C 569	12.4	42.8	17	6	AR433858	Sequence	AR433858	Sequence	12.2	42.1	25	6	BD217278
C 570	12.4	42.8	20	6	AR087472	Sequence	AR087472	Sequence	12.2	42.1	25	6	BD217278
C 571	12.4	42.8	20	6	AR110661	Sequence	AR110661	Sequence	12.2	42.1	25	6	BD217278
C 572	12.4	42.8	20	6	AR154578	Sequence	AR154578	Sequence	12.2	42.1	25	6	BD217278
C 573	12.4	42.8	20	6	AR287624	Sequence	AR287624	Sequence	12.2	42.1	25	6	BD217278
C 574	12.4	42.8	20	6	BD088479	A method	BD088479 A method	Sequence	12.2	42.1	25	6	BD217278
C 575	12.4	42.8	20	12	AB069208	Synthetic	AB069208 Synthetic	Sequence	12.2	42.1	25	6	BD217278
C 576	12.4	42.8	21	6	BD090087	A method	BD090087 A method	Sequence	12.2	42.1	25	6	BD217278

650	12.2	42.1	49	8	AJ599937	AJ599937 Arabidops	C 723	12	41.4	31	6	AR072430	AR072430 Sequence
C 651	12.2	42.1	51	6	A07731	A07731 Oligonucleo	C 724	12	41.4	31	6	126541	126541 Sequence
C 652	12.2	42.1	51	6	A10029	A10029 Nucleotide	C 725	12	41.4	31	6	AR342577	AR342577 Sequence
C 653	12.2	42.1	51	6	AR009025	AR009025 Sequence	C 726	12	41.4	31	6	AX425752	AX425752 Sequence
C 654	12.2	42.1	51	6	AR052680	AR052680 Sequence	C 727	12	41.4	31	6	AX582577	AX582577 Sequence
C 655	12.2	42.1	51	6	AR060991	AR060991 Sequence	C 728	12	41.4	33	6	AR119805	AR119805 Sequence
C 656	12.2	42.1	51	6	AR087722	AR087722 Sequence	C 729	12	41.4	33	6	BD243338	BD243338 Improved
C 657	12.2	42.1	51	6	AR175113	AR175113 Sequence	C 730	12	41.4	33	6	AR344239	AR344239 Sequence
C 658	12.2	42.1	51	6	AR174699	AR174699 Sequence	C 731	12	41.4	33	6	AR361666	AR361666 Sequence
C 659	12.2	42.1	51	6	AR287993	AR287993 Sequence	C 732	12	41.4	33	6	AX021816	AX021816 Sequence
C 660	12.2	42.1	51	6	AR360127	AR360127 Sequence	C 733	12	41.4	33	6	AX137248	AX137248 Sequence
C 661	12.2	42.1	51	6	AX115765	AX115765 Sequence	C 734	12	41.4	33	6	BD015172	BD015172 Continuou
C 662	12.2	42.1	51	6	AX157907	AX157907 Sequence	C 735	12	41.4	33	6	BD094291	BD094291 A prepara
C 663	12.2	42.1	51	6	AR261804	AR261804 Sequence	C 736	12	41.4	33	6	BD179370	BD179370 A novel p
C 664	12.2	42.1	54	6	AR268146	AR268146 Sequence	C 737	12	41.4	33	10	MDTRVJNK	X63559 M.domesticu
C 665	12.2	42.1	54	6	AX009656	AX009656 Sequence	C 738	12	41.4	34	6	AR225312	AR225312 Sequence
C 666	12.2	42.1	54	6	AX010918	AX010918 Sequence	C 739	12	41.4	34	6	BD062172	BD062172 Expresio
C 667	12.2	42.1	55	6	AP206138	AP206138 Rana chap	C 740	12	41.4	35	6	AX768186	AX768186 Sequence
C 668	12.2	42.1	55	6	AX484741	AX484741 Sequence	C 741	12	41.4	36	6	I36659	I36659 Sequence
C 669	12.2	42.1	56	6	AX9113897	AX9113897 Sequence	C 742	12	41.4	36	6	AR204491	AR204491 Sequence
C 670	12.2	42.1	56	6	BD049430	BD049430 Sequence	C 743	12	41.4	36	6	AR218089	AR218089 Sequence
C 671	12.2	42.1	57	8	AJ589198	AJ589198 Arabidops	C 744	12	41.4	36	6	AR230460	AR230460 Sequence
C 672	12.2	42.1	57	9	S73835	S73835 TCR V gamma	C 745	12	41.4	36	6	AR310155	AR310155 Sequence
C 673	12.2	42.1	60	6	AR116980	AR116980 Sequence	C 746	12	41.4	36	6	AR350567	AR350567 Sequence
C 674	12.2	42.1	60	6	AR201880	AR201880 Sequence	C 747	12	41.4	36	6	BD218702	BD218702 DNA-damag
C 675	12.2	42.1	60	6	AR204376	AR204376 Sequence	C 748	12	41.4	37	6	AX220013	AX220013 Sequence
C 676	12.2	42.1	60	6	BD136895	BD136895 Method of	C 749	12	41.4	37	6	AX220055	AX220055 Sequence
C 677	12.2	42.1	61	12	SYNAPAP	M60085 Avian neovi	C 750	12	41.4	37	6	AX425077	AX425077 Sequence
C 678	12.2	42.1	61	6	AR238676	AR238676 Sequence	C 751	12	41.4	37	6	AX581633	AX581633 Sequence
C 679	12.2	42.1	62	6	BD182107	BD182107 von Willeb	C 752	12	41.4	37	6	AX581705	AX581705 Sequence
C 680	12.2	42.1	63	6	AX892522	AX892522 Sequence	C 753	12	41.4	37	6	AX768141	AX768141 Sequence
C 681	12.2	42.1	63	6	BD034785	BD034785 Sequence	C 754	12	41.4	38	6	A84834	A84834 Sequence
C 682	12.2	42.1	65	6	AX483163	AX483163 Sequence	C 755	12	41.4	38	6	AR339693	AR339693 Sequence
C 683	12.2	42.1	65	6	AX484957	AX484957 Sequence	C 756	12	41.4	38	6	AX089641	AX089641 Sequence
C 684	12.2	42.1	65	6	AX486035	AX486035 Sequence	C 757	12	41.4	38	6	BD082282	BD082282 Modified
C 685	12.2	42.1	69	6	AX920653	AX920653 Sequence	C 758	12	41.4	40	6	AX306333	AX306333 Sequence
C 686	12.2	42.1	69	6	BD056186	BD056186 Sequence	C 759	12	41.4	40	6	AX452098	AX452098 Sequence
C 687	12.2	42.1	70	8	YSCMTOR12A	M34152 S.cerevisia	C 760	12	41.4	40	6	AX496010	AX496010 Sequence
C 688	12.2	42.1	73	6	E02131	E02131 Pseudoknot	C 761	12	41.4	40	9	HSZ74585	Z74585 H.sapiens j
C 689	12.2	42.1	75	6	AX919319	AX919319 Sequence	C 762	12	41.4	40	10	MDTRVJNA	X63579 M.domesticu
C 690	12.2	42.1	75	6	BD054852	BD054852 Arabidops	C 763	12	41.4	41	6	BD259967	BD259967 Polynucle
C 691	12.2	42.1	76	11	AL954623	AL954623 Arabidops	C 764	12	41.4	41	6	AR179776	AR179776 Sequence
C 692	12.2	42.1	77	9	HUMDF1747	M99847 Human anti g	C 765	12	41.4	41	6	AR253879	AR253879 Sequence
C 693	12.2	42.1	78	8	AJ588412	AJ588412 Arabidops	C 766	12	41.4	41	6	AR410230	AR410230 Sequence
C 694	12.2	42.1	80	5	F225878S.1	AF225888 Gallus ga	C 767	12	41.4	41	6	AX045453	AX045453 Sequence
C 695	12.2	42.1	80	6	AX904773	AX904773 Sequence	C 768	12	41.4	41	6	AX045800	AX045800 Sequence
C 696	12.2	42.1	80	6	BD040306	BD040306 Sequence	C 769	12	41.4	41	6	AX316543	AX316543 Sequence
C 697	12.2	42.1	80	8	AJ589320	AJ589320 Arabidops	C 770	12	41.4	41	6	AX515635	AX515635 Sequence
C 698	12.2	42.1	80	8	ARH521333	AJ521333 Arabidops	C 771	12	41.4	41	6	AX518230	AX518230 Sequence
C 699	12.2	42.1	80	8	ARH521704	AJ521704 Arabidops	C 772	12	41.4	41	6	AX776705	AX776705 Sequence
C 700	12.2	42.1	80	11	HUMSWX1361	L41964 Human chrom	C 773	12	41.4	41	6	AX786980	AX786980 Sequence
C 701	12.2	42.1	88	6	AX661812	AX661812 Sequence	C 774	12	41.4	42	6	AX068408	AX068408 Sequence
C 702	12.2	41.4	18	6	BD009430	BD009430 Probes, m	C 775	12	41.4	42	6	AX225222	AX225222 Sequence
C 703	12.2	41.4	19	6	AX130174	AX130174 Sequence	C 776	12	41.4	42	8	ATHS30885	AJ530885 Arabidops
C 704	12.2	41.4	21	6	AR299259	AR299259 Sequence	C 777	12	41.4	43	6	AX04415	A04415 Oligonucleo
C 705	12.2	41.4	22	6	E26475	E26475 Erysipeloth	C 778	12	41.4	43	14	S39353S1	S39353 glycoprotei
C 706	12.2	41.4	23	6	AX546629	AX546629 Sequence	C 779	12	41.4	44	6	AR009755	AR009755 Sequence
C 707	12.2	41.4	24	6	AX444040	AX444040 Sequence	C 780	12	41.4	44	6	I73486	I73486 Sequence
C 708	12.2	41.4	25	6	AR206010	AR206010 Sequence	C 781	12	41.4	44	6	I81195	I81195 Sequence
C 709	12.2	41.4	25	6	AX042765	AX042765 Sequence	C 782	12	41.4	44	6	AX225221	AX225221 Sequence
C 710	12.2	41.4	25	6	AX042937	AX042937 Sequence	C 783	12	41.4	44	10	MMRFHDRNA	X60921 M.musculus
C 711	12.2	41.4	25	6	AX043006	AX043006 Sequence	C 784	12	41.4	45	6	AX494453	AX494453 Sequence
C 712	12.2	41.4	25	6	AX043316	AX043316 Sequence	C 785	12	41.4	46	10	MDTRVJNC	X63581 M.domesticu
C 713	12.2	41.4	25	6	AX043699	AX043699 Sequence	C 786	12	41.4	46	10	MDTRVJNC	AR168818 Sequence
C 714	12.2	41.4	25	6	AX610025	AX610025 Sequence	C 787	12	41.4	47	6	I27812	I27812 Sequence
C 715	12.2	41.4	25	6	AX616244	AX616244 Sequence	C 788	12	41.4	47	6	AR200287	AR200287 Sequence
C 716	12.2	41.4	25	6	AX616245	AX616245 Sequence	C 789	12	41.4	47	6	AR262419	AR262419 Sequence
C 717	12.2	41.4	25	6	AX616246	AX616246 Sequence	C 790	12	41.4	47	6	AR288324	AR288324 Sequence
C 718	12.2	41.4	25	6	AX616247	AX616247 Sequence	C 791	12	41.4	47	6	AR289750	AR289750 Sequence
C 719	12.2	41.4	26	6	AX100410	AX100410 Sequence	C 792	12	41.4	47	6	AR291617	AR291617 Sequence
C 720	12.2	41.4	29	6	E13950	E13950 PCR primer	C 793	12	41.4	47	6	AX378366	AX378366 Sequence
C 721	12.2	41.4	30	6	AX791834	AX791834 Sequence	C 794	12	41.4	47	6	BD196599	BD196599 Prostatic
C 722	12.2	41.4	30	6	AX793345	AX793345 Sequence	C 795	12	41.4	48	6	AR032579	AR032579 Sequence

796	12	41.4	48	6	I29319	Sequence 19	11.8	40.7	20	6	AR112667	Sequence
797	12	41.4	48	6	I90993	Sequence 19	11.8	40.7	20	6	AR353716	Sequence
798	12	41.4	48	6	AR209243	Sequence	11.8	40.7	20	6	AR082340	Sequence
799	12	41.4	50	6	I29594	Sequence 46	11.8	40.7	20	6	BD003455	Sequence
800	12	41.4	50	6	I29594	Sequence 46	11.8	40.7	20	6	BD003455	Sequence
801	12	41.4	50	6	I91268	Sequence 46	11.8	40.7	23	6	E09974	Primer for
802	12	41.4	50	6	AR209518	Sequence	11.8	40.7	23	6	E10118	PCR primer
803	12	41.4	51	6	AR203936	Sequence	11.8	40.7	23	6	I00179	Sequence 3
804	12	41.4	51	6	AR204251	Sequence	11.8	40.7	23	6	AX017118	Sequence
805	12	41.4	51	10	MDTRVNJD	XG3582 M.domesticu	11.8	40.7	23	6	AX350159	Sequence
806	12	41.4	51	10	AF328707	Mus muscu	11.8	40.7	23	6	AX017118	Sequence
807	12	41.4	52	6	AX301290	Sequence	11.8	40.7	24	6	AX065817	Sequence
808	12	41.4	52	6	BD036823	Sequence	11.8	40.7	24	6	AX119458	Sequence
809	12	41.4	53	6	AX498443	Sequence	11.8	40.7	24	6	AX493975	Sequence
810	12	41.4	53	6	HE3345051	AJ345051 hederia he	11.8	40.7	24	6	AX494078	Sequence
811	12	41.4	54	5	AF206133	Paa spino	11.8	40.7	25	6	AR016133	Sequence
812	12	41.4	54	5	AF206160	Limmonect	11.8	40.7	25	6	AR019131	Sequence
813	12	41.4	54	6	AR064484	Sequence	11.8	40.7	25	6	AR434685	Sequence
814	12	41.4	54	6	AR081483	Sequence	11.8	40.7	25	6	AX042557	Sequence
815	12	41.4	54	6	AX494274	Sequence	11.8	40.7	25	6	AX042587	Sequence
816	12	41.4	54	6	AX494279	Sequence	11.8	40.7	25	6	AX042625	Sequence
817	12	41.4	54	10	AX177453	AX177453 Mus muscu	11.8	40.7	25	6	AX042935	Sequence
818	12	41.4	54	10	AX177476	AX177476 Mus muscu	11.8	40.7	25	6	AX042963	Sequence
819	12	41.4	55	6	AX899466	Sequence	11.8	40.7	25	6	AX043040	Sequence
820	12	41.4	55	6	BD034999	Sequence	11.8	40.7	25	6	AX043147	Sequence
821	12	41.4	58	6	AX314166	Sequence	11.8	40.7	25	6	AX043173	Sequence
822	12	41.4	58	6	BD496999	Sequence	11.8	40.7	25	6	AX043220	Sequence
823	12	41.4	59	6	AX011462	Sequence	11.8	40.7	25	6	AX043294	Sequence
824	12	41.4	59	6	BD225753	Screening	11.8	40.7	25	6	AX043310	Sequence
825	12	41.4	60	6	AX521521	Sequence	11.8	40.7	25	6	AX043311	Sequence
826	12	41.4	60	12	SYNANVAA	M50029 Avian neovi	11.8	40.7	25	6	AX043439	Sequence
827	12	41.4	61	11	HSUB4975	U84975 Homo sapien	11.8	40.7	25	6	AX043479	Sequence
828	12	41.4	65	6	AX306322	Sequence	11.8	40.7	25	6	AX043492	Sequence
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DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274240
VERSION BD274240.1 GI:33084008
KEYWORDS JP 2002526030-A/207.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL Patent: JP 2002526030-A 207 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/207
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
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source
LOCUS BD274240 46 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274240
VERSION BD274240.1 GI:33084017
KEYWORDS JP 2002526030-A/216.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL Patent: JP 2002526030-A 216 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/216
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274252
VERSION BD274252.1 GI:33084020
KEYWORDS JP 2002526030-A/219.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL Patent: JP 2002526030-A 219 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/219
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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LOCUS BD274253 46 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274253
VERSION BD274253.1 GI:33084021
KEYWORDS JP 2002526030-A/220.

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C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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DEFINITION Identification of molecular interaction sites in RNA for novel drug
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ACCESSION BD274252
VERSION BD274252.1 GI:33084020
KEYWORDS JP 2002526030-A/219.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL Patent: JP 2002526030-A 219 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/219
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
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source
LOCUS BD274253 46 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274253
VERSION BD274253.1 GI:33084021
KEYWORDS JP 2002526030-A/220.

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SOURCE          synthetic construct
ORGANISM         synthetic construct
REFERENCE        1 (bases 1 to 46)
AUTHORS         Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE           Identification of molecular interaction sites in RNA for novel drug
JOURNAL         discovery
COMMENT         Patent: JP 2002526030-A 220 20-AUG-2002;
                ISIS PHARMACEUTICALS INC
                OS Artificial Sequence
                PN JP 2002526030-A/220
                PD 20-AUG-2002
                PF 12-MAY-1999 JP 2000548510
                PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
                KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
                C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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                Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;
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                DB 19 TATGATTCCTTTTGTAAAGCCCTAGGGGC 46
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                LOCUS Identification of molecular interaction sites in RNA for novel drug
                DEFINITION discovery.
                ACCESSION BD274257
                VERSION BD274257.1 GI:33084025
                KEYWORDS JP 2002526030-A/224.
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                REFERENCE 1 (bases 1 to 46)
                AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
                TITLE Identification of molecular interaction sites in RNA for novel drug
                JOURNAL discovery
                COMMENT Patent: JP 2002526030-A 224 20-AUG-2002;
                ISIS PHARMACEUTICALS INC
                OS Artificial Sequence
                PN JP 2002526030-A/224
                PD 20-AUG-2002
                PF 12-MAY-1999 JP 2000548510
                PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
                KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
                C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;
QY 1 UAUGAUUUUUUUUAAGCCCUAGGGGC 28
DB 19 TATGATTCCTTTTGTAAAGCCCTAGGGGC 46
RESULT 8
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LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274265
VERSION BD274265.1 GI:33084033
KEYWORDS JP 2002526030-A/232.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 232 20-AUG-2002;
                ISIS PHARMACEUTICALS INC
                OS Artificial Sequence
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                PD 20-AUG-2002
                PF 12-MAY-1999 JP 2000548510
                PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
                KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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                Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;
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                LOCUS Identification of molecular interaction sites in RNA for novel drug
                DEFINITION discovery.
                ACCESSION BD274268
                VERSION BD274268.1 GI:33084036
                KEYWORDS JP 2002526030-A/235.
                SOURCE synthetic construct
                ORGANISM synthetic construct
                REFERENCE 1 (bases 1 to 46)
                AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
                TITLE Identification of molecular interaction sites in RNA for novel drug
                JOURNAL discovery
                COMMENT Patent: JP 2002526030-A 235 20-AUG-2002;
                ISIS PHARMACEUTICALS INC
                OS Artificial Sequence
                PN JP 2002526030-A/235
                PD 20-AUG-2002
                PF 12-MAY-1999 JP 2000548510
                PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI

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DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC
C12Q1/68, A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description
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ORIGIN

Query Match 96.6%; Score 28; DB 6; Length 46;
Best Local Similarity 60.7%; Pred. No. 0.061;
Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10

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LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.

ACCESSION

BD274269 1 GI:33084037

VERSION

JP 2002526030-A/236.

KEYWORDS

synthetic construct

SOURCE

artificial construct

ORGANISM

artificial sequences.

REFERENCE

1 (bases 1 to 46)

AUTHORS

Ecker, D.J., Sampath, R., Griffey, R. and Mcneil, J.

TITLE

Identification of molecular interaction sites in RNA for novel drug

JOURNAL

Patent: JP 2002526030-A 236 20-AUG-2002;

COMMENT

ISIS PHARMACEUTICALS INC

OS

Artificial Sequence

PN

JP 2002526030-A/236

PD

20-AUG-2002

PF

12-MAY-1998 JP 2000548510

PR

12-MAY-1998 US 60/085092, 12-MAY-1998 US 09/076440 PI

DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC

C12Q1/68, A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description

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Location/Qualifiers

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ORIGIN

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Best Local Similarity 60.7%; Pred. No. 0.061;

Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

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DB 19 TATGATTCCTTTTGTAGCCCTAGGGGC 46

KEYWORDS

synthetic construct

SOURCE

artificial construct

REFERENCE

1 (bases 1 to 42)

AUTHORS

Ecker, D.J., Sampath, R., Griffey, R. and Mcneil, J.

TITLE

Identification of molecular interaction sites in RNA for novel drug

JOURNAL

Patent: JP 2002526030-A 237 20-AUG-2002;

COMMENT

ISIS PHARMACEUTICALS INC

OS

Artificial Sequence

PN

JP 2002526030-A/237

PD

20-AUG-2002

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12-MAY-1998 JP 2000548510

PR

12-MAY-1998 US 60/085092, 12-MAY-1998 US 09/076440 PI

DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC

C12Q1/68, A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description

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Matches 16; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

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DB 4 TAGATTCCTTTTGTAGCCCTAGGGCT 32

RESULT 12

BD274278

LOCUS Identification of molecular interaction sites in RNA for novel drug

DEFINITION discovery.

ACCESSION BD274278.1 GI:33084046

VERSION JP 2002526030-A/245.

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 42)

Ecker, D.J., Sampath, R., Griffey, R. and Mcneil, J.

Identification of molecular interaction sites in RNA for novel drug

discovery

Patent: JP 2002526030-A 245 20-AUG-2002;

ISIS PHARMACEUTICALS INC

OS Artificial Sequence

PN JP 2002526030-A/245

PD 20-AUG-2002

PF 12-MAY-1998 JP 2000548510

PR 12-MAY-1998 US 60/085092, 12-MAY-1998 US 09/076440 PI

DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC

C12Q1/68, A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description

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Location/Qualifiers

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ORIGIN

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Matches 16; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

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Db 4 TAAGATTCTTTTGTAAAGCCCTACGGCT 32

RESULT 13
BD274238
LOCUS BD274238 46 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.

ACCESSION BD274238.1 GI:33084006
VERSION BD274238.1
KEYWORDS JP 2002526030-A/205.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 46)
Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
TITLE discovery

JOURNAL Patent: JP 2002526030-A 205 20-AUG-2002;

COMMENT
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/205
PD 20-AUG-2002

PF 12-MAY-1999 JP 2000548510
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DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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ORIGIN

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DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.

ACCESSION BD274256.1 GI:33084024
VERSION BD274256.1
KEYWORDS JP 2002526030-A/223.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 46)
Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
TITLE discovery

JOURNAL Patent: JP 2002526030-A 223 20-AUG-2002;

COMMENT
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/223
PD 20-AUG-2002

PF 12-MAY-1999 JP 2000548510

PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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Best Local Similarity 57.1%; Pred. No. 1.8;
Matches 16; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUUAAGCCCUAGGGGC 28
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Db 19 TAAGATTCTTTTGTAAAGCCCTACGGGC 46

RESULT 15

BD274271
LOCUS BD274271 42 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.

ACCESSION BD274271.1 GI:33084039
VERSION BD274271.1
KEYWORDS JP 2002526030-A/238.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 42)
Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
TITLE discovery

JOURNAL Patent: JP 2002526030-A 238 20-AUG-2002;

COMMENT
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/238
PD 20-AUG-2002

PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence PH Key

Location/Qualifiers
FT source 1..42
/organism='Artificial Sequence'.
FT

FEATURES
source

1..42
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 82.1%; Score 23.8; DB 6; Length 42;
Best Local Similarity 55.6%; Pred. No. 5.3;
Matches 15; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUUUUUUUAAGCCCUAGGGG 27
: |||:||||:|||||:|||||:|||||:
Db 4 TAAGATTCTTTTGTAAAGCCCTACGGC 30

RESULT 16

BD274279
LOCUS BD274279 42 bp RNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.

ACCESSION

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VERSION BD274279.1 GI:33084047
KEYWORDS JP 2002526030-A/246.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 246 20-AUG-2002;
COMMENT OS Artificial Sequence
PN JP 2002526030-A/246
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
CI2Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..42
FT /organism='Artificial Sequence'.

FEATURES
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/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 82.1%; Score 23.8; DB 6; Length 42;
Best Local Similarity 55.6%; Pred. No. 5.3;
Matches 15; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUCUUUUUGAAGCCUAGGGG 27
:|||||:|||||:|||||:|||||
4 TAAGATCTTTTGTAAAGCCCTAGGCG 30

RESULT 17
BD274247
LOCUS 46 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274247.1 GI:33084015
VERSION BD274247.1 GI:33084015
KEYWORDS JP 2002526030-A/214.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 214 20-AUG-2002;
COMMENT OS Artificial Sequence
PN JP 2002526030-A/214
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
CI2Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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FT /organism='Artificial Sequence'.

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Query Match 82.1%; Score 23.8; DB 6; Length 46;
Best Local Similarity 55.6%; Pred. No. 5.2;
Matches 15; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUCUUUUUGAAGCCUAGGGG 27
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19 TAAGATCTTTTGTAAAGCCCTAGGCG 45

RESULT 19
BD274272
LOCUS 42 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274272.1 GI:33084040
VERSION BD274272.1 GI:33084040
KEYWORDS JP 2002526030-A/239.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 239 20-AUG-2002;
COMMENT OS Artificial Sequence
PN JP 2002526030-A/239
PD 20-AUG-2002

FEATURES
source
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/mol_type="genomic RNA"
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ORIGIN

Query Match 82.1%; Score 23.8; DB 6; Length 46;
Best Local Similarity 55.6%; Pred. No. 5.2;
Matches 15; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUCUUUUUGAAGCCUAGGGG 27
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19 TAAGATCTTTTGTAAAGCCCTAGGCG 45

RESULT 19
BD274272
LOCUS 42 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274272.1 GI:33084040
VERSION BD274272.1 GI:33084040
KEYWORDS JP 2002526030-A/239.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 239 20-AUG-2002;
COMMENT OS Artificial Sequence
PN JP 2002526030-A/239
PD 20-AUG-2002

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/db_xref="taxon:32630"

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PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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FT /organism='Artificial Sequence'.
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/db_xref='taxon:32630'
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Query Match 80.0%; Score 23.2; DB 6; Length 42;
Best Local Similarity 57.1%; Pred. No. 9.9;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUCUUUUUGUAGCCCUAGGGGCU 29
Db 5 AAGATTCCTTTTGTAAAGCCCAAGGGCT 32
RESULT 20
BD274273 42 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274273
VERSION BD274273.1 GI:33084041
KEYWORDS JP 2002526030-A/240.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 240 20-AUG-2002;
COMMENT OS PHARMACEUTICALS INC
PN JP 2002526030-A/240
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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source
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/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
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Best Local Similarity 57.1%; Pred. No. 9.9;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUCUUUUUGUAGCCCUAGGGGCU 29
Db 5 AAGATTCCTTTTGTAAAGCCCAAGGGCT 32
RESULT 21
BD274280 42 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.

ACCESSION BD274280
VERSION BD274280.1 GI:33084048
KEYWORDS JP 2002526030-A/247.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 247 20-AUG-2002;
COMMENT OS PHARMACEUTICALS INC
PN JP 2002526030-A/247
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..42
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Best Local Similarity 57.1%; Pred. No. 9.9;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUCUUUUUGUAGCCCUAGGGGCU 29
Db 5 AAGATTCCTTTTGTAAAGCCCAAGGGCT 32
RESULT 22
BD274281 42 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274281
VERSION BD274281.1 GI:33084049
KEYWORDS JP 2002526030-A/248.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 248 20-AUG-2002;
COMMENT OS PHARMACEUTICALS INC
PN JP 2002526030-A/248
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..42
FT /organism='Artificial Sequence'.
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source
1..42
/organism='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'
ORIGIN


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discovery.
ACCESSION      BD274243
VERSION        BD274243.1 GI:33084011
KEYWORDS       JP 2002526030-A/210.
SOURCE         synthetic construct
ORGANISM       synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE      Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS       Identification of molecular interaction sites in RNA for novel drug
TITLE         discovery
JOURNAL       Patent: JP 2002526030-A 210 20-AUG-2002;
COMMENT       ISIS PHARMACEUTICALS INC
LOCUS         OS Artificial Sequence
DEFINITION    PN JP 2002526030-A/210
PF 20-AUG-2002
PR 12-MAY-1999 JP 2000548510
PI 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
KEYWORDS      DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
SOURCE        C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence PH Key
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/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 29;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUUUUUUUUUAAGCCUAGGGGC 28
| | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
Db 20 AAGATCTTTTGTAAAGCCCAAGGC 46

RESULT 27
BD274258
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274258.1 GI:33084026
VERSION BD274258
KEYWORDS JP 2002526030-A/225.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
TITLE discovery
JOURNAL Patent: JP 2002526030-A 225 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
LOCUS OS Artificial Sequence
DEFINITION PN JP 2002526030-A/225
PF 20-AUG-2002
PR 12-MAY-1999 JP 2000548510
PI 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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of Artificial Sequence: Novel Sequence PH Key
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ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 29;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUUUUUUUUUAAGCCUAGGGGC 28
| | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
Db 20 AAGATCTTTTGTAAAGCCCAAGGC 46

RESULT 28
BD274259
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274259.1 GI:33084027
VERSION BD274259
KEYWORDS JP 2002526030-A/226.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
TITLE discovery
JOURNAL Patent: JP 2002526030-A 226 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
LOCUS OS Artificial Sequence
DEFINITION PN JP 2002526030-A/226
PF 20-AUG-2002
PR 12-MAY-1999 JP 2000548510
PI 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 29;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUUUUUUUUUAAGCCUAGGGGC 28
| | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
Db 20 AAGATCTTTTGTAAAGCCCAAGGC 46

RESULT 29
BD274260
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274260.1 GI:33084028
VERSION BD274260
KEYWORDS JP 2002526030-A/227.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
TITLE discovery
JOURNAL Patent: JP 2002526030-A 227 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
LOCUS OS Artificial Sequence
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PN JP 2002526030-A/227
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Location/Qualifiers
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Location/Qualifiers
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/db_xref='taxon:32630'
ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 29;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
Qy 2 AUGAUCUUUUUGAAGCCCUAGGGGC 28
|:::|:::|:::|:::|:::|:::|:::|
Db 20 AAGATTCCTTTCTGTAAGCCCTACGGGC 46

RESULT 30
BD274246
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION
BD274246
ACCESSION BD274246.1 GI:33084014
VERSION JP 2002526030-A/213.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 46)
REFERENCE
1 Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 213 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/213
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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/organism='Artificial Sequence'.
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Location/Qualifiers
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/db_xref='taxon:32630'
ORIGIN
Query Match 74.5%; Score 21.6; DB 6; Length 46;
Best Local Similarity 53.6%; Pred. No. 54;
Matches 15; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
Qy 1 UGAUCUUUUUGAAGCCCUAGGGGC 28
|:::|:::|:::|:::|:::|:::|:::|
Db 19 TTGATCCTTTCTGTAAGCCCTACGGGC 46

RESULT 31
BD274248
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION
BD274248
ACCESSION BD274248.1 GI:33084016
VERSION JP 2002526030-A/215.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 46)
REFERENCE
1 Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 215 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/215
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
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FEATURES
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1..46
Location/Qualifiers
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Best Local Similarity 53.6%; Pred. No. 54;
Matches 15; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
Qy 1 UGAUCUUUUUGAAGCCCUAGGGGC 28
|:::|:::|:::|:::|:::|:::|:::|
Db 19 TTGATCCTTTCTGTAAGCCCTACGGGC 46

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DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274248
VERSION BD274248.1 GI:33084016
KEYWORDS JP 2002526030-A/215.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE
1 Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 215 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/215
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
/organism='Artificial Sequence'.
FEATURES
source
1..46
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Query Match 74.5%; Score 21.6; DB 6; Length 46;
Best Local Similarity 53.6%; Pred. No. 54;
Matches 15; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
Qy 1 UGAUCUUUUUGAAGCCCUAGGGGC 28
|:::|:::|:::|:::|:::|:::|:::|
Db 19 TTGATCCTTTCTGTAAGCCCTACGGGC 46

RESULT 32
BD274262
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION
BD274262
ACCESSION BD274262.1 GI:33084030
VERSION JP 2002526030-A/229.
KEYWORDS synthetic construct
SOURCE synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE
1 Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 229 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/229
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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of Artificial Sequence: Novel Sequence FH Key
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ACCESSION BD274262.1 GI:33084030
VERSION JP 2002526030-A/229.
KEYWORDS synthetic construct
SOURCE synthetic construct
artificial sequences.
1 (bases 1 to 46)
REFERENCE
1 Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
AUTHORS Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 229 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/229
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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DEFINITION Identification of molecular interaction sites in RNA for novel drug
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ACCESSION BD274282
VERSION BD274282.1 GI:33084050
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SOURCE synthetic construct
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REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 249 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
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PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Search completed: April 18, 2004, 08:41:23
Job time : 765.333 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 05:09:18 ; Search time 746.333 Seconds
(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1774092

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a

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C 136	11.2	38.6	55	3	S55610S2	S55612 Broad-Compl	C 209	10.8	37.2	35	6	AX020425	AX020425 Sequence
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C 217	10.8	37.2	45	6	AR032518	AR032518 Sequence	C 290	10.6	36.6	41	6	AX520728	AX520728 Sequence
C 218	10.8	37.2	45	6	AR032730	AR032730 Sequence	C 291	10.6	36.6	43	6	BD142503	BD142503 A method
C 219	10.8	37.2	45	6	I29258	I29258 Sequence 13	C 292	10.6	36.6	43	6	BD142503	BD142503 A method
C 220	10.8	37.2	45	6	I29470	I29470 Sequence 13	C 293	10.6	36.6	43	6	ATH553793	ATH553793 Arabidops
C 221	10.8	37.2	45	6	I30932	I30932 Sequence 34	C 294	10.6	36.6	44	5	GU34614	GU34614 Gallus gall
C 222	10.8	37.2	45	6	I91144	I91144 Sequence 34	C 295	10.6	36.6	47	6	AR290538	AR290538 Sequence
C 223	10.8	37.2	45	6	AR209182	AR209182 Sequence	C 296	10.6	36.6	48	13	S76577	S76577 TCR alpha =
C 224	10.8	37.2	45	6	AR209394	AR209394 Sequence	C 297	10.6	36.6	50	6	AR164552	AR164552 Sequence
C 225	10.8	37.2	47	6	AR290551	AR290551 Sequence	C 298	10.6	36.6	54	6	A57940	A57940 Sequence 6
C 226	10.8	37.2	47	6	AR291810	AR291810 Sequence	C 299	10.6	36.6	55	8	AJ588102	AJ588102 Arabidops
C 227	10.8	37.2	48	6	I15164	I15164 Sequence 13	C 300	10.6	36.6	60	6	A38757	A38757 Sequence 7
C 228	10.8	37.2	50	6	A21306	A21306 Nucleotide	C 301	10.6	36.6	60	6	I89875	I89875 Sequence 7
C 229	10.8	37.2	50	6	AR033731	AR033731 Sequence	C 302	10.6	36.6	60	10	MUSHPRT5	K01511 Mus musculus
C 230	10.8	37.2	50	6	AR064653	AR064653 Sequence	C 303	10.6	36.6	63	6	AX384573	AX384573 Sequence
C 231	10.8	37.2	50	6	BD273138	BD273138 Oral immu	C 304	10.6	36.6	64	6	AX270680	AX270680 Sequence
C 232	10.8	37.2	50	6	I29471	I29471 Sequence 34	C 305	10.6	36.6	64	6	AX272211	AX272211 Sequence
C 233	10.8	37.2	50	6	I91145	I91145 Sequence 34	C 306	10.6	36.6	65	6	AX485715	AX485715 Sequence
C 234	10.8	37.2	50	6	AR209395	AR209395 Sequence	C 307	10.6	36.6	65	6	AX486452	AX486452 Sequence
C 235	10.8	37.2	51	6	AR009025	AR009025 Sequence	C 308	10.6	36.6	66	1	ECOLETX	M17101 E.coli heat
C 236	10.8	37.2	51	6	AR052680	AR052680 Sequence	C 309	10.6	36.6	68	5	AF125363	AF125363 Polyodon
C 237	10.8	37.2	51	6	AR060991	AR060991 Sequence	C 310	10.6	36.6	69	6	AR171551	AR171551 Sequence
C 238	10.8	37.2	51	6	AR087722	AR087722 Sequence	C 311	10.6	36.6	69	6	BD005571	BD005571 Compositi
C 239	10.8	37.2	51	6	AX175113	AX175113 Sequence	C 312	10.6	36.6	70	6	AX315526	AX315526 Sequence
C 240	10.8	37.2	51	6	I74699	I74699 Sequence 39	C 313	10.6	36.6	70	6	BD051059	BD051059 Sequence
C 241	10.8	37.2	51	6	AR287993	AR287993 Sequence	C 314	10.6	36.6	71	10	MMU403504	AJ403504 M.musculus
C 242	10.8	37.2	51	6	AR360127	AR360127 Sequence	C 315	10.6	36.6	72	1	ECOPKYD2	M30729 E.coli/IS1
C 243	10.8	37.2	51	6	AX117401	AX117401 Sequence	C 316	10.6	36.6	73	8	AY203293	AY203293 Arabidops
C 244	10.8	37.2	51	6	AX118033	AX118033 Sequence	C 317	10.6	36.6	78	9	AY256011	AY256011 Macaca mu
C 245	10.8	37.2	51	6	AX190386	AX190386 Sequence	C 318	10.4	35.9	17	6	AX217417	AX217417 Sequence
C 246	10.8	37.2	53	10	MUSTCBYBH	M36462 Mouse T-cel	C 319	10.4	35.9	17	6	AX217784	AX217784 Sequence
C 247	10.8	37.2	58	10	MUSTCBYBH	M36460 Mouse T-cel	C 320	10.4	35.9	17	6	AX218162	AX218162 Sequence
C 248	10.8	37.2	58	10	MUSTCBYBG	M36459 Mouse T-cel	C 321	10.4	35.9	17	6	AX304795	AX304795 Sequence
C 249	10.8	37.2	59	10	MUSTCBYBJ	M36463 Mouse T-cel	C 322	10.4	35.9	20	6	AR293822	AR293822 Sequence
C 250	10.8	37.2	61	6	AR355618	AR355618 Sequence	C 323	10.4	35.9	20	6	AR350263	AR350263 Sequence
C 251	10.8	37.2	62	10	MUSTCBYBE	M36457 Mouse T-cel	C 324	10.4	35.9	21	6	AR096878	AR096878 Sequence
C 252	10.8	37.2	65	6	AX483200	AX483200 Sequence	C 325	10.4	35.9	24	6	AX445741	AX445741 Sequence
C 253	10.8	37.2	65	6	AX485901	AX485901 Sequence	C 326	10.4	35.9	25	8	ATH526250	AJ526250 Arabidops
C 254	10.8	37.2	65	6	AX486309	AX486309 Sequence	C 327	10.4	35.9	25	8	ATH526284	AJ526284 Arabidops
C 255	10.8	37.2	68	8	ATH521374	AJ521374 Arabidops	C 328	10.4	35.9	27	6	AR091453	AR091453 Sequence
C 256	10.8	37.2	72	11	AL806183	AL806183 Arabidops	C 329	10.4	35.9	27	6	BD000823	BD000823 Amplifica
C 257	10.8	37.2	77	8	AJ593524	AY93524 Arabidops	C 330	10.4	35.9	27	6	BD166181	BD166181 Amplifica
C 258	10.6	36.6	23	6	E09974	E09974 Primer for	C 331	10.4	35.9	28	8	ATH522549	AJ522549 Arabidops
C 259	10.6	36.6	23	6	E30118	E30118 PCR primer	C 332	10.4	35.9	29	6	AR096942	AR096942 Sequence
C 260	10.6	36.6	24	6	E58779	E58779 Novel human	C 333	10.4	35.9	29	6	BD136137	BD136137 Vaccines
C 261	10.6	36.6	24	6	AX768391	AX768391 Sequence	C 334	10.4	35.9	30	6	AX155197	AX155197 Sequence
C 262	10.6	36.6	28	6	AX027376	AX027376 Sequence	C 335	10.4	35.9	30	6	BD061572	BD061572 D-aminoac
C 263	10.6	36.6	29	6	E05018	E05018 Primer. 9/1	C 336	10.4	35.9	30	9	HUMPLTP09	U37816 Human phosph
C 264	10.6	36.6	30	6	AR079815	AR079815 Sequence	C 337	10.4	35.9	31	6	BD002393	BD002393 Gene comp
C 265	10.6	36.6	30	6	AR182366	AR182366 Sequence	C 338	10.4	35.9	31	6	BD002854	BD002854 Gene comp
C 266	10.6	36.6	30	6	AX321657	AX321657 Sequence	C 339	10.4	35.9	36	6	A14290	A14290 oligonucleo
C 267	10.6	36.6	30	6	AX793354	AX793354 Sequence	C 340	10.4	35.9	36	6	AX14291	A14291 oligonucleo
C 268	10.6	36.6	30	6	BD014351	BD014351 Plant pro	C 341	10.4	35.9	36	6	AX770369	AX770369 Sequence
C 269	10.6	36.6	31	6	AX274078	AX274078 Sequence	C 342	10.4	35.9	36	6	AX805507	AX805507 Sequence
C 270	10.6	36.6	31	6	AX274083	AX274083 Sequence	C 343	10.4	35.9	36	6	AX805508	AX805508 Sequence
C 271	10.6	36.6	31	6	AX274267	AX274267 Sequence	C 344	10.4	35.9	36	6	AX805508	AX805508 Sequence
C 272	10.6	36.6	31	6	AX425824	AX425824 Sequence	C 345	10.4	35.9	39	6	AX576868	AX576868 Sequence
C 273	10.6	36.6	31	6	AX425978	AX425978 Sequence	C 346	10.4	35.9	39	6	AX576868	AX576868 Sequence
C 274	10.6	36.6	31	6	AX426018	AX426018 Sequence	C 347	10.4	35.9	40	6	AR211425	AR211425 Sequence
C 275	10.6	36.6	31	6	AX426065	AX426065 Sequence	C 348	10.4	35.9	40	6	AX001534	AX001534 Sequence
C 276	10.6	36.6	31	6	AX582413	AX582413 Sequence	C 349	10.4	35.9	40	6	AX001546	AX001546 Sequence
C 277	10.6	36.6	31	6	AX582509	AX582509 Sequence	C 350	10.4	35.9	41	6	AR083451	AR083451 Sequence
C 278	10.6	36.6	31	6	AX582707	AX582707 Sequence	C 351	10.4	35.9	41	6	AX515077	AX515077 Sequence
C 279	10.6	36.6	31	6	AX582713	AX582713 Sequence	C 352	10.4	35.9	41	6	AX517004	AX517004 Sequence
C 280	10.6	36.6	31	6	AX582742	AX582742 Sequence	C 353	10.4	35.9	41	6	AX518661	AX518661 Sequence
C 281	10.6	36.6	34	6	AX774183	AX774183 Sequence	C 354	10.4	35.9	41	6	AX518935	AX518935 Sequence
C 282	10.6	36.6	34	6	AX923320	AX923320 Sequence	C 355	10.4	35.9	41	6	AX518936	AX518936 Sequence
C 283	10.6	36.6	35	6	A47631	A47631 Sequence 8	C 356	10.4	35.9	41	6	AX519515	AX519515 Sequence
C 284	10.6	36.6	35	6	I82275	I82275 Sequence 8	C 357	10.4	35.9	41	6	AX521064	AX521064 Sequence

C 358	10.4	35.9	43	6	AX483586	AX483586 Sequence	C 431	10.2	35.2	24	6	BD141353	BD141353 Novel phi
C 359	10.4	35.9	45	10	MMTCRA235	X70719 M. musculus	C 432	10.2	35.2	24	6	BD142847	BD142847 Novel G P
C 360	10.4	35.9	47	6	AR288398	AR288398 Sequence	C 433	10.2	35.2	24	6	BD170822	BD170822 Process F
C 361	10.4	35.9	47	6	AR288695	AR288695 Sequence	C 434	10.2	35.2	24	6	BD181657	BD181657 Novel phi
C 362	10.4	35.9	47	6	AR288999	AR288999 Sequence	C 435	10.2	35.2	25	6	BD245582	BD245582 Developme
C 363	10.4	35.9	47	6	AR291157	AR291157 Sequence	C 436	10.2	35.2	25	6	BD472516	BD472516 Sequence
C 364	10.4	35.9	47	6	AR291884	AR291884 Sequence	C 437	10.2	35.2	26	6	BD177543	BD177543 Method fo
C 365	10.4	35.9	47	6	AX378367	AX378367 Sequence	C 438	10.2	35.2	29	6	AX394123	AX394123 Sequence
C 366	10.4	35.9	50	6	AR437951	AR437951 Sequence	C 439	10.2	35.2	30	6	AS6993	AS6993 Sequence 51
C 367	10.4	35.9	50	6	AX303593	AX303593 Sequence	C 440	10.2	35.2	30	6	AR054072	AR054072 Sequence
C 368	10.4	35.9	50	6	AX910776	AX910776 Sequence	C 441	10.2	35.2	30	6	ARI27461	ARI27461 Sequence
C 369	10.4	35.9	51	6	BD046309	BD046309 Sequence	C 442	10.2	35.2	30	6	I39960	I39960 Sequence 13
C 370	10.4	35.9	51	6	AX158923	AX158923 Sequence	C 443	10.2	35.2	30	6	AX474312	AX474312 Sequence
C 371	10.4	35.9	51	6	AX158924	AX158924 Sequence	C 444	10.2	35.2	31	6	AR072430	AR072430 Sequence
C 372	10.4	35.9	51	6	AX162574	AX162574 Sequence	C 445	10.2	35.2	31	6	I26541	I26541 Sequence 23
C 373	10.4	35.9	55	6	AR426960	AR426960 Sequence	C 446	10.2	35.2	33	6	ARI194376	ARI194376 Sequence
C 374	10.4	35.9	55	6	BD122513	BD122513 EST and e	C 447	10.2	35.2	33	6	AX060364	AX060364 Sequence
C 375	10.4	35.9	57	6	AX437963	AX437963 Sequence	C 448	10.2	35.2	33	6	AX069219	AX069219 Sequence
C 376	10.4	35.9	57	6	AX303606	AX303606 Sequence	C 449	10.2	35.2	33	6	AX069219	AX069219 Sequence
C 377	10.4	35.9	59	6	AX684263	AX684263 Sequence	C 450	10.2	35.2	33	6	AX329399	AX329399 Sequence
C 378	10.4	35.9	59	6	AX905506	AX905506 Sequence	C 451	10.2	35.2	34	9	AF505532	AF505532 Homo sapi
C 379	10.4	35.9	59	6	BD041039	BD041039 Sequence	C 452	10.2	35.2	35	6	I81895	I81895 Sequence 4
C 380	10.4	35.9	60	6	AR437964	AR437964 Sequence	C 453	10.2	35.2	36	6	AX464538	AX464538 Sequence
C 381	10.4	35.9	60	6	AX303607	AX303607 Sequence	C 454	10.2	35.2	38	6	ARI46220	ARI46220 Sequence
C 382	10.4	35.9	60	10	MMU86744	UB6744 Mus musculus	C 455	10.2	35.2	38	6	AR307789	AR307789 Sequence
C 383	10.4	35.9	61	6	AR437950	AR437950 Sequence	C 456	10.2	35.2	39	6	AX1997	AX1997 Synthetic I
C 384	10.4	35.9	61	6	AX303592	AX303592 Sequence	C 457	10.2	35.2	39	6	AX494814	AX494814 Sequence
C 385	10.4	35.9	67	6	AX920548	AX920548 Sequence	C 458	10.2	35.2	40	6	AX167345	AX167345 Sequence
C 386	10.4	35.9	67	6	BD056081	BD056081 Sequence	C 459	10.2	35.2	40	6	AX452098	AX452098 Sequence
C 387	10.4	35.9	68	5	AB096004	AB096004 Trachurus	C 460	10.2	35.2	41	6	AX514276	AX514276 Sequence
C 388	10.4	35.9	68	5	AF125364	AF125364 Acipenser	C 461	10.2	35.2	41	6	AX515172	AX515172 Sequence
C 389	10.4	35.9	68	5	AF125365	AF125365 Acipenser	C 462	10.2	35.2	41	6	AX517966	AX517966 Sequence
C 390	10.4	35.9	68	5	AF125366	AF125366 Acipenser	C 463	10.2	35.2	41	6	AX520458	AX520458 Sequence
C 391	10.4	35.9	68	5	AF125367	AF125367 Acipenser	C 464	10.2	35.2	41	6	AX521154	AX521154 Sequence
C 392	10.4	35.9	68	5	AF125368	AF125368 Acipenser	C 465	10.2	35.2	42	6	AR079470	AR079470 Sequence
C 393	10.4	35.9	68	5	AF125369	AF125369 Acipenser	C 466	10.2	35.2	44	6	AX804136	AX804136 Sequence
C 394	10.4	35.9	68	5	AF125370	AF125370 Scaphirhy	C 467	10.2	35.2	45	6	AR003527	AR003527 Sequence
C 395	10.4	35.9	68	5	AF125371	AF125371 Scaphirhy	C 468	10.2	35.2	45	6	AR079762	AR079762 Sequence
C 396	10.4	35.9	68	5	AF125372	AF125372 Scaphirhy	C 469	10.2	35.2	45	6	AR081292	AR081292 Sequence
C 397	10.4	35.9	70	7	PMUPBN	PMUPBN	C 470	10.2	35.2	45	6	ARI170652	ARI170652 Sequence
C 398	10.4	35.9	70	7	PMUPBN	PMUPBN	C 471	10.2	35.2	45	6	I55640	I55640 Sequence 4
C 399	10.4	35.9	71	6	AR058848	AR058848 Sequence	C 472	10.2	35.2	45	9	HS274591	HS274591 H. sapiens j
C 400	10.4	35.9	71	6	AR063574	AR063574 Sequence	C 473	10.2	35.2	46	6	AR160662	AR160662 Sequence
C 401	10.4	35.9	71	6	ARI40964	ARI40964 Sequence	C 474	10.2	35.2	46	6	BD238290	BD238290 Accelerat
C 402	10.4	35.9	73	10	F322144S30	AF322173 Mus muscu	C 475	10.2	35.2	46	6	BD238290	BD238290 Accelerat
C 403	10.4	35.9	75	4	E01677	E01677 DNA sequenc	C 476	10.2	35.2	46	6	E17006	E17006 Primer. 7/1
C 404	10.4	35.9	77	6	E01806	E01806 DNA encodin	C 477	10.2	35.2	46	6	E17038	E17038 Primer. 7/1
C 405	10.4	35.9	77	6	E01808	E01808 DNA encodin	C 478	10.2	35.2	46	6	E17049	E17049 Sequence
C 406	10.4	35.9	77	6	E01808	E01808 DNA encodin	C 479	10.2	35.2	47	6	AR288951	AR288951 Sequence
C 407	10.4	35.9	77	6	E02146	E02146 DNA encodin	C 480	10.2	35.2	47	6	AR289362	AR289362 Sequence
C 408	10.4	35.9	77	6	E02398	E02398 DNA encodin	C 481	10.2	35.2	48	6	AR289436	AR289436 Sequence
C 409	10.4	35.9	77	6	AR362673	AR362673 Sequence	C 482	10.2	35.2	48	6	AR032579	AR032579 Sequence
C 410	10.4	35.9	78	3	AY013980	AY013980 Eupriat	C 483	10.2	35.2	48	6	I29319	I29319 Sequence 19
C 411	10.4	35.9	78	6	AX362675	AX362675 Sequence	C 484	10.2	35.2	48	6	AR009243	AR009243 Sequence 19
C 412	10.4	35.9	78	8	AX596509	AX596509 Arabidops	C 485	10.2	35.2	48	9	S81456	S81456 T cell anti
C 413	10.2	35.2	20	6	AR156531	AR156531 Sequence	C 486	10.2	35.2	49	6	E54534	E54534 Herpesvirus
C 414	10.2	35.2	20	6	AR226170	AR226170 Sequence	C 487	10.2	35.2	50	6	AR003085	AR003085 Sequence
C 415	10.2	35.2	20	6	AX929255	AX929255 Sequence	C 488	10.2	35.2	50	6	AR003178	AR003178 Sequence
C 416	10.2	35.2	21	6	AR299973	AR299973 Sequence	C 489	10.2	35.2	50	6	AR009028	AR009028 Sequence
C 417	10.2	35.2	22	6	AR139340	AR139340 Sequence	C 490	10.2	35.2	50	6	AR011152	AR011152 Sequence
C 418	10.2	35.2	22	6	AX645165	AX645165 Sequence	C 491	10.2	35.2	50	6	AR032854	AR032854 Sequence
C 419	10.2	35.2	22	6	AX377060	AX377060 Sequence	C 492	10.2	35.2	50	6	AR052683	AR052683 Sequence
C 420	10.2	35.2	23	6	AX377063	AX377063 Sequence	C 493	10.2	35.2	50	6	AR060994	AR060994 Sequence
C 421	10.2	35.2	23	6	AX377066	AX377066 Sequence	C 494	10.2	35.2	50	6	AR087725	AR087725 Sequence
C 422	10.2	35.2	23	6	AX546629	AX546629 Sequence	C 495	10.2	35.2	50	6	ARI75116	ARI75116 Sequence
C 423	10.2	35.2	24	6	AR361510	AR361510 Sequence	C 496	10.2	35.2	50	6	I17790	I17790 Sequence 19
C 424	10.2	35.2	24	6	AX389401	AX389401 Sequence	C 497	10.2	35.2	50	6	I19215	I19215 Sequence 35
C 425	10.2	35.2	24	6	AX290262	AX290262 Sequence	C 498	10.2	35.2	50	6	I20056	I20056 Sequence 19
C 426	10.2	35.2	24	6	AX291190	AX291190 Sequence	C 499	10.2	35.2	50	6	I29594	I29594 Sequence 42
C 427	10.2	35.2	24	6	AX922534	AX922534 Sequence	C 500	10.2	35.2	50	6	I74702	I74702 Sequence 42
C 428	10.2	35.2	24	6	AX444424	AX444424 Sequence	C 501	10.2	35.2	50	6	I91268	I91268 Sequence 46
C 429	10.2	35.2	24	6	AX539017	AX539017 Sequence	C 502	10.2	35.2	50	6	AR209518	AR209518 Sequence
C 430	10.2	35.2	24	6	BD013015	BD013015 Novel G P	C 503	10.2	35.2	50	6	AR287996	AR287996 Sequence

796	9.8	33.8	20	6	AX293788	AX293788 Sequence	C 869	9.8	33.8	30	6	A23000	A23000 CASOL14 oli
797	9.8	33.8	20	6	BD137620	BD137620 Mutation	C 870	9.8	33.8	30	6	AR007186	AR007186 Sequence
798	9.8	33.8	21	6	BD213600	BD213600 Chromosom	C 871	9.8	33.8	30	6	AR034002	AR034002 Sequence
C 799	9.8	33.8	21	6	AR362466	AR362466 Sequence	C 872	9.8	33.8	30	6	AR048089	AR048089 Sequence
800	9.8	33.8	21	6	AR367675	AR367675 Sequence	C 873	9.8	33.8	30	6	AR054193	AR054193 Sequence
801	9.8	33.8	21	6	AX098565	AX098565 Sequence	C 874	9.8	33.8	30	6	AR063953	AR063953 Sequence
C 802	9.8	33.8	21	6	AX318288	AX318288 Sequence	C 875	9.8	33.8	30	6	AR124011	AR124011 Sequence
803	9.8	33.8	21	6	AX805191	AX805191 Sequence	C 876	9.8	33.8	30	6	BD269922	BD269922 Compositi
C 804	9.8	33.8	22	6	E29427	E29427 Oligonucleo	C 877	9.8	33.8	30	6	E58504	E58504 CMTF/IL-6 c
805	9.8	33.8	22	6	AR219168	AR219168 Sequence	C 878	9.8	33.8	30	6	I23896	I23896 Sequence 13
806	9.8	33.8	22	6	AX174308	AX174308 Sequence	C 879	9.8	33.8	30	6	I47741	I47741 Sequence 13
C 807	9.8	33.8	22	6	AX147378	AX147378 Sequence	C 880	9.8	33.8	30	6	I74402	I74402 Sequence 4
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C 809	9.8	33.8	23	6	E49313	E49313 Infectious	C 882	9.8	33.8	30	6	AR359148	AR359148 Sequence
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ALIGNMENTS
RESULT 1
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LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274270
VERSION BD274270.1 GI:33084038
KEYWORDS JP 2002526030-A/237.
SOURCE synthetic construct

BD274270 42 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274271
VERSION BD274271.1 GI:33084039
KEYWORDS JP 2002526030-A/238.
SOURCE synthetic construct
ORGANISM
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL
COMMENT Patent: JP 2002526030-A 238 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/238
PD 20-AUG-2002
PP 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092 12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
CI2Q1/69,A61K31/7105,A61K48/00,CI2N15/09,CI2N15/00 CC Description
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Db 7 GATTCCTTTGTGAAGCCCTACGGG 30

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LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274271
VERSION BD274271.1 GI:33084039
KEYWORDS JP 2002526030-A/238.
SOURCE synthetic construct
ORGANISM
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL
COMMENT Patent: JP 2002526030-A 238 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/238
PD 20-AUG-2002
PP 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092 12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
CI2Q1/69,A61K31/7105,A61K48/00,CI2N15/09,CI2N15/00 CC Description
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Best Local Similarity 54.2%; Pred.No. 5.6;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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ORGANISM    synthetic construct
REFERENCE    artificial sequences.
1 (bases 1 to 42)
AUTHORS     Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE       Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL     Patent: JP 2002526030-A 245 20-AUG-2002;
COMMENT     ISIS PHARMACEUTICALS INC
OS          Artificial Sequence
PN          JP 2002526030-A/245
PD          20-AUG-2002
PF          12-MAY-1999 JP 2000548510
PR          12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Db 7 GATTCCTTTTGTAGCCCTACGGG 30
RESULT 7
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LOCUS
DEFINITION
Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274279
VERSION 1 GI:33084047
KEYWORDS JP 2002526030-A/246.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 246 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/246
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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Best Local Similarity 54.2%; Pred. No. 5.6;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Db 7 GATTCCTTTTGTAGCCCTACGGG 30

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Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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LOCUS
DEFINITION
Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274280
VERSION 1 GI:33084048
KEYWORDS JP 2002526030-A/247.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 247 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/247
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
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Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Db 7 GATTCCTTTTGTAGCCCTACGGG 30
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LOCUS
DEFINITION
Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274281
VERSION 1 GI:33084049
KEYWORDS JP 2002526030-A/248.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 248 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/248
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI

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RESULT 13
BD274238 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274238
VERSION BD274238.1 GI:33084006
KEYWORDS JP 2002526030-A/205.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 205 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/205
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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RESULT 14
BD274240 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274240

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VERSION BD274240.1 GI:33084008
KEYWORDS JP 2002526030-A/207.
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 207 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/207
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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BD274241 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274241
VERSION BD274241.1 GI:33084009
KEYWORDS JP 2002526030-A/208.
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 208 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/208
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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ACCESSION BD274247
VERSION BD274247.1 GI:33084015
KEYWORDS JP 2002526030-A/214.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 214 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/214
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAGCCCNANGNG 27
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DB 22 GATCTTTTGTAGCCCTAGGGG 45

RESULT 20
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LOCUS BD274248
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274248
VERSION BD274248.1 GI:33084016
KEYWORDS JP 2002526030-A/215.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 215 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/215
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Best Local Similarity 54.2%; Pred. No. 5.6;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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DB 22 GATCTTTTGTAGCCCTAGGGG 45
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Best Local Similarity 54.2%; Pred. No. 5.6;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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DB 22 GATCTTTTGTAGCCCTAGGGG 45

RESULT 21
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LOCUS BD274249
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274249
VERSION BD274249.1 GI:33084017
KEYWORDS JP 2002526030-A/216.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 216 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/216
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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DB 22 GATCTTTTGTAGCCCTAGGGG 45

RESULT 22
BD274252
LOCUS BD274252
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274252
VERSION BD274252.1 GI:33084020
KEYWORDS JP 2002526030-A/219.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 219 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/219
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discovery.
BD274256
BD274256.1 GI:33084024
JP 2002526030-A/223.
synthetic construct
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artificial sequences.
1 (bases 1 to 46)
Ecker,D.J., Sampath,R., Griffey,R. and McNeil,J.
Identification of molecular interaction sites in RNA for novel drug
discovery
Patent: JP 2002526030-A 223 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/223
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.
ACCESSION BD274257
VERSION BD274257.1 GI:33084025
KEYWORDS JP 2002526030-A/224.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and McNeil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug discovery
JOURNAL Patent: JP 2002526030-A 224 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
         OS Artificial Sequence
         PN JP 2002526030-A/224
         PD 20-AUG-2002
         PF 12-MAY-1999 JP 2000548510
         PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
         DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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DB      22 GATCTTTTGTAAAGCCCTAGCGG 45

RESULT 31
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DEFINITION Identification of molecular interaction sites in RNA for novel drug
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ACCESSION  BD274264
VERSION     1 GI:33084032
KEYWORDS   JP 2002526030-A/231.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
            1 (bases 1 to 46)
REFERENCE  Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
            Identification of molecular interaction sites in RNA for novel drug
            discovery
            Patent: JP 2002526030-A 231 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
            OS Artificial Sequence
            PN JP 2002526030-A/231
            PD 20-AUG-2002
            PF 12-MAY-1999 JP 2000548510
            PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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DB      22 GATCTTTTGTAAAGCCCTACGGG 45

RESULT 32
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LOCUS      46 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
            discovery.
ACCESSION  BD274265
VERSION     1 GI:33084033
KEYWORDS   JP 2002526030-A/232.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
            1 (bases 1 to 46)
REFERENCE  Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
            Identification of molecular interaction sites in RNA for novel drug
            discovery
            Patent: JP 2002526030-A 232 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
            Journal

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ACCESSION BD274276
VERSION BD274276.1 GI:33084044
KEYWORDS JP 2002526030-A/243.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug discovery

JOURNAL Patent: JP 2002526030-A 243 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/243
PD 20-AUG-2002 JP 2000548510
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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RESULT 40
BD274274
LOCUS 42 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.

ACCESSION BD274274
VERSION BD274274.1 GI:33084042
KEYWORDS JP 2002526030-A/241.
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug discovery

JOURNAL Patent: JP 2002526030-A 241 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/241
PD 20-AUG-2002 JP 2000548510
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Job time : 775.333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: April 18, 2004, 05:05:34 ; Search time 179.667 Seconds
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Title: US-09-310-844C-23

Perfect score: 29

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Total number of hits satisfying chosen parameters: 3399856

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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3: Geneseqn2000s:*

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5: Geneseqn2001bs:*

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7: Geneseqn2003as:*

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9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	18	62.1	42	3	AAA71128
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8	18	62.1	42	3	AAA71113
9	18	62.1	42	3	AAA71124
10	18	62.1	42	3	AAA71132
11	18	62.1	42	3	AAA71120
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13	18	62.1	42	3	AAA71118
14	18	62.1	42	3	AAA71119
15	18	62.1	42	3	AAA71126
16	18	62.1	42	3	AAA71131
17	18	62.1	42	3	AAA71127
18	18	62.1	42	3	AAA71116
19	18	62.1	42	3	AAA71115
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26	18	62.1	45	3	AAA70825	AAA70825	Molecular
27	18	62.1	45	3	AAA70824	AAA70824	Molecular
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33	18	62.1	46	3	AAA71095	AAA71095	Molecular
34	18	62.1	46	3	AAA71106	AAA71106	Molecular
35	18	62.1	46	3	AAA71107	AAA71107	Molecular
36	18	62.1	46	3	AAA71109	AAA71109	Molecular
37	18	62.1	46	3	AAA71087	AAA71087	Molecular
38	18	62.1	46	3	AAA71093	AAA71093	Molecular
39	18	62.1	46	3	AAA71096	AAA71096	Molecular
40	18	62.1	46	3	AAA71099	AAA71099	Molecular
41	18	62.1	46	3	AAA71088	AAA71088	Molecular
42	18	62.1	46	3	AAA71100	AAA71100	Molecular
43	18	62.1	46	3	AAA71105	AAA71105	Molecular
44	18	62.1	46	3	AAA71103	AAA71103	Molecular
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46	18	62.1	46	3	AAA71104	AAA71104	Molecular
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52	13	44.8	42	3	AAA71130	AAA71130	Molecular
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54	13	44.8	42	3	AAA71122	AAA71122	Molecular
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59	12.2	42.1	30	6	ABX68475	ABX68475	Novel Hel
60	12.2	42.1	50	6	ABZ00473	ABZ00473	Human leu
61	12.2	42.1	55	2	AAQ37152	AAQ37152	Probe to
62	12.2	42.1	60	6	ABN37080	ABN37080	Human spl
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88	11.8	40.7	77	4	AAV01050	AAV01050	Synthetic
89	11.8	40.7	77	6	AAV22494	AAV22494	F3R3F1 pr
90	11.8	40.7	77	6	AAV22495	AAV22495	F3R32 pr1
91	11.6	40.0	24	7	ACC69357	ACC69357	IS45/46 p
92	11.6	40.0	24	9	AAV58606	AAV58606	p45/46sf1
93	11.6	40.0	31	6	ABK21678	ABK21678	Human ERG
94	11.6	40.0	31	7	ABZ65562	ABZ65562	Human HBR
95	11.6	40.0	31	7	ACD65561	ACD65561	HCV minus
96	11.6	40.0	31	7	ACD60488	ACD60488	HCV DNAsy

97	11.6	40.0	33	5	AAH48524	Aah48524 Human TNF	c 170	11.2	38.6	40	4	AAE81504	Aaf81504 Novel hum
98	11.6	40.0	38	9	ADD71328	Ad71328 Maize S-a	c 171	11.2	38.6	40	4	AAE87604	Aaf87604 DNA assoc
99	11.6	40.0	40	6	AB221055	Ab221055 Transduc	c 172	11.2	38.6	41	6	AB233378	Abs33378 pBAdmyc/h
100	11.6	40.0	41	6	AB221054	Ab221054 Transduc	c 173	11.2	38.6	41	6	AB260089	Ab260089 Human DNA
101	11.6	40.0	41	6	AB248772	Ab248772 Human ald	c 174	11.2	38.6	41	6	AB260026	Ab260026 Human DNA
102	11.6	40.0	41	6	AB246261	Ab246261 Human ald	c 175	11.2	38.6	41	6	AB246360	Ab246360 Human ald
103	11.6	40.0	42	6	ABN83483	Abn83483 Murine MC	c 176	11.2	38.6	41	6	AB248872	Ab248872 Human ald
104	11.6	40.0	42	6	ABN16938	Abn16938 E. coli e	c 177	11.2	38.6	41	10	AB248872	Ab248872 Human ald
105	11.6	40.0	56	4	ABN42033	Abn42033 Human spl	c 178	11.2	38.6	43	3	AAZ57795	Aaz57795 Antisense
106	11.6	40.0	60	6	ABN40005	Abn40005 Human spl	c 179	11.2	38.6	47	3	AAZ57795	Aaz57795 Antisense
107	11.6	40.0	60	6	ABN33033	Abn33033 Human spl	c 180	11.2	38.6	47	3	AAH88320	Aah88320 CNS disor
108	11.6	40.0	65	6	ABN52087	Abn52087 Mouse spl	c 181	11.2	38.6	50	4	AAH88320	Aah88320 CNS disor
109	11.6	40.0	65	6	ABN57170	Abn57170 Mouse spl	c 182	11.2	38.6	50	4	AAH88320	Aah88320 CNS disor
110	11.6	40.0	69	7	ACF42757	Acf42757 shMOG gen	c 183	11.2	38.6	50	6	ABZ07540	Abz07540 Human leu
111	11.6	40.0	69	7	ABL54573	AbL54573 Mouse per	c 184	11.2	38.6	50	6	ABZ07540	Abz07540 Human leu
112	11.4	39.3	17	7	ACC52535	Acc52535 Human tum	c 185	11.2	38.6	50	6	ABZ03951	Abz03951 Human leu
113	11.4	39.3	17	7	ABT34657	Abt34657 Tumour su	c 186	11.2	38.6	50	6	ABZ04880	Abz04880 Human leu
114	11.4	39.3	20	2	AAZ04979	Aaz04979 PCR prime	c 187	11.2	38.6	50	6	ABZ06777	Abz06777 Human leu
115	11.4	39.3	25	8	AC105200	Ac105200 Human mic	c 188	11.2	38.6	51	4	AAZ13164	Aaz13164 Human SNP
116	11.4	39.3	25	8	AC105201	Ac105201 Human mic	c 189	11.2	38.6	51	4	AAZ13164	Aaz13164 Human SNP
117	11.4	39.3	25	8	AC194430	Ac194430 Human mic	c 190	11.2	38.6	52	2	AAV69331	Aav69331 Human LIR
118	11.4	39.3	31	3	AAZ87592	Aaz87592 Mouse CD1	c 191	11.2	38.6	52	2	AAV69331	Aav69331 Human LIR
119	11.4	39.3	31	3	AAZ87589	Aaz87589 Human CD1	c 192	11.2	38.6	56	4	AAZ09291	Aaz09291 RNA seque
120	11.4	39.3	36	2	AAZ47031	Aaz47031 CD40 liga	c 193	11.2	38.6	60	1	AAZ09291	Aaz09291 RNA seque
121	11.4	39.3	40	6	ABD27069	Abd27069 Plasmid p	c 194	11.2	38.6	60	6	ABN49506	Abn49506 Coliphage
122	11.4	39.3	41	6	AB154588	Ab154588 Human pro	c 195	11.2	38.6	60	6	ABN49506	Abn49506 Coliphage
123	11.4	39.3	44	3	AAZ71108	Aaz71108 Molecular	c 196	11.2	38.6	60	6	ABN47240	Abn47240 Human spl
124	11.4	39.3	44	4	ABF82920	Abf82920 CD154 ext	c 197	11.2	38.6	65	6	ABN47240	Abn47240 Human spl
125	11.4	39.3	44	4	ABK89864	Abk89864 Binding d	c 198	11.2	38.6	65	6	ABN30679	Abn30679 Rat splc
126	11.4	39.3	44	9	ADD25467	Add25467 Binding d	c 199	11.2	38.6	65	6	ABN30679	Abn30679 Rat splc
127	11.4	39.3	46	3	AAZ71092	Aaz71092 Molecular	c 200	11.2	38.6	65	6	ABN31177	Abn31177 Rat splc
128	11.4	39.3	46	6	ABN72001	Abn72001 Streptoco	c 201	11.2	38.6	70	5	AAF29242	Aaf29242 Ligand to
129	11.4	39.3	49	6	ABN71758	Abn71758 Streptoco	c 202	11.2	38.6	70	5	AAF29242	Aaf29242 Ligand to
130	11.4	39.3	49	6	ABN46181	Abn46181 ccdB gene	c 203	11.2	38.6	78	9	ABE85488	AbE85488 Farnesyl
131	11.4	39.3	51	4	AAZ29026	Aaz29026 Human SNP	c 204	11	37.9	17	7	ABT35710	Abt35710 Tumour su
132	11.4	39.3	51	4	AAH79850	Aah79850 Human DNA	c 205	11	37.9	17	7	ABT35710	Abt35710 Tumour su
133	11.4	39.3	60	6	ABK36336	Abk36336 HIV DNA e	c 206	11	37.9	17	7	ABT36438	Abt36438 Tumour su
134	11.4	39.3	60	6	ABN47785	Abn47785 Human spl	c 207	11	37.9	17	7	ABT36438	Abt36438 Tumour su
135	11.4	39.3	60	6	ABN33454	Abn33454 Human spl	c 208	11	37.9	17	7	ABT36438	Abt36438 Tumour su
136	11.4	39.3	60	6	ABN35172	Abn35172 Human spl	c 209	11	37.9	25	8	ACC59745	Acc59745 S suis ar
137	11.4	39.3	65	2	AAV36558	Aav36558 DNA subet	c 210	11	37.9	29	3	AAZ44211	Aaz44211 Murine CD
138	11.4	39.3	65	6	ABN31992	Abn31992 Rat splc	c 211	11	37.9	29	3	AAZ44211	Aaz44211 Murine CD
139	11.2	38.6	20	6	AB193874	Ab193874 Capture o	c 212	11	37.9	30	6	AAV05611	Aav05611 Primer fo
140	11.2	38.6	24	6	AB184319	Ab184319 Capture o	c 213	11	37.9	30	6	ABK14828	Abk14828 Rat FGF-R
141	11.2	38.6	24	6	AB192761	Ab192761 Capture o	c 214	11	37.9	30	6	ABK14828	Abk14828 Rat FGF-R
142	11.2	38.6	24	6	AB182565	Ab182565 Capture o	c 215	11	37.9	31	2	AAQ56641	Aaq56641 PCR prime
143	11.2	38.6	24	6	AB182565	Ab182565 Capture o	c 216	11	37.9	31	2	AAQ56641	Aaq56641 PCR prime
144	11.2	38.6	24	6	AB192760	Ab192760 Capture o	c 217	11	37.9	31	2	AAQ56641	Aaq56641 PCR prime
145	11.2	38.6	24	6	AB192760	Ab192760 Capture o	c 218	11	37.9	31	2	AAQ56641	Aaq56641 PCR prime
146	11.2	38.6	24	6	AB182564	Ab182564 Capture o	c 219	11	37.9	31	2	AAQ56641	Aaq56641 PCR prime
147	11.2	38.6	24	6	AB191831	Ab191831 Capture o	c 220	11	37.9	31	2	AAQ56641	Aaq56641 PCR prime
148	11.2	38.6	24	8	ACF04473	Acf04473 Real time	c 221	11	37.9	31	2	AAQ56641	Aaq56641 PCR prime
149	11.2	38.6	25	3	AAZ29218	Aaz29218 Sindbis v	c 222	11	37.9	31	2	AAQ56641	Aaq56641 PCR prime
150	11.2	38.6	25	3	AAZ29218	Aaz29218 Sindbis v	c 223	11	37.9	31	2	AAQ56641	Aaq56641 PCR prime
151	11.2	38.6	25	3	AAZ29218	Aaz29218 Sindbis v	c 224	11	37.9	31	2	AAQ56641	Aaq56641 PCR prime
152	11.2	38.6	25	3	AAZ29218	Aaz29218 Sindbis v	c 225	11	37.9	31	2	AAQ56641	Aaq56641 PCR prime
153	11.2	38.6	25	8	ACK30015	Ack30015 Human mic	c 226	10.8	37.2	17	7	ABT36384	Abt36384 Tumour su
154	11.2	38.6	25	8	ACK30015	Ack30015 Human mic	c 227	10.8	37.2	17	7	ABT36384	Abt36384 Tumour su
155	11.2	38.6	25	8	ACK30015	Ack30015 Human mic	c 228	10.8	37.2	17	7	ABT36384	Abt36384 Tumour su
156	11.2	38.6	30	2	AAQ70868	Aaq70868 Target se	c 229	10.8	37.2	17	7	ABT36384	Abt36384 Tumour su
157	11.2	38.6	30	2	AAQ70868	Aaq70868 Target se	c 230	10.8	37.2	17	7	ABT36384	Abt36384 Tumour su
158	11.2	38.6	32	4	AAZ92791	Aaz92791 Real time	c 231	10.8	37.2	17	7	ABT36384	Abt36384 Tumour su
159	11.2	38.6	32	4	AAZ92791	Aaz92791 Real time	c 232	10.8	37.2	17	7	ABT36384	Abt36384 Tumour su
160	11.2	38.6	33	3	AAZ92792	Aaz92792 Sindbis v	c 233	10.8	37.2	17	7	ABT36384	Abt36384 Tumour su
161	11.2	38.6	33	3	AAZ92792	Aaz92792 Sindbis v	c 234	10.8	37.2	17	7	ABT36384	Abt36384 Tumour su
162	11.2	38.6	33	6	AAZ92792	Aaz92792 Sindbis v	c 235	10.8	37.2	17	7	ABT36384	Abt36384 Tumour su
163	11.2	38.6	33	6	AAZ92792	Aaz92792 Sindbis v	c 236	10.8	37.2	17	7	ABT36384	Abt36384 Tumour su
164	11.2	38.6	34	2	AAV90805	Aav90805 Primer Y2	c 237	10.8	37.2	20	4	AAH4608	Aah4608 Novel mou
165	11.2	38.6	34	2	AAV90805	Aav90805 Primer Y2	c 238	10.8	37.2	20	4	AAH4608	Aah4608 Novel mou
166	11.2	38.6	36	2	AAV02487	Aav02487 Bridge MP	c 239	10.8	37.2	22	6	ABE59032	AbE59032 Human G-p
167	11.2	38.6	36	2	AAV02487	Aav02487 Bridge MP	c 240	10.8	37.2	22	6	ABE59032	AbE59032 Human G-p
168	11.2	38.6	37	9	ADC24312	Adc24312 PCR prime	c 241	10.8	37.2	22	6	ABQ88567	Abq88567 Human GPC
169	11.2	38.6	37	9	ADC24312	Adc24312 PCR prime	c 242	10.8	37.2	22	6	ABQ88567	Abq88567 Human GPC

c 243	10.8	37.2	22	5	ABQ88570	Abq88570 Human GPC	316	10.8	37.2	60	6	ABN50045	Abn50045 Human spl
c 244	10.8	37.2	23	3	AAQ99238	Aaa99238 Human pho	c 317	10.8	37.2	60	6	ABN42062	Abn42062 Human spl
c 245	10.8	37.2	24	3	ACF03497	Adc03497 Oryza sat	c 318	10.8	37.2	60	6	ABN36609	Abn36609 Human spl
c 246	10.8	37.2	25	4	AAV90566	Aav90566 Forward p	c 319	10.8	37.2	61	6	ABN32506	Abn32506 Human spl
c 247	10.8	37.2	25	4	AAH39727	Aah39727 SNP speci	c 320	10.8	37.2	61	6	AAV76047	Aav76047 Staphyloc
c 248	10.8	37.2	25	5	AA522104	Aas22104 Human COL	c 321	10.8	37.2	64	7	AB217788	Ab217788 S2 subtra
c 249	10.8	37.2	25	6	AB575571	Ab575571 Human PAP	c 322	10.8	37.2	65	6	AB229118	Ab229118 Candida g
c 250	10.8	37.2	25	6	AB575578	Ab575578 Human PAP	c 323	10.8	37.2	65	6	AB229526	Ab229526 Candida g
c 251	10.8	37.2	25	6	AB575577	Ab575577 Human PAP	c 324	10.8	37.2	65	6	AB226621	Ab226621 Candida e
c 252	10.8	37.2	25	6	AB575573	Ab575573 Human PAP	c 325	10.8	37.2	65	6	ABN57271	Abn57271 Mouse spl
c 253	10.8	37.2	25	6	AB575572	Ab575572 Human PAP	c 326	10.8	37.2	65	6	ABN57807	Abn57807 Mouse spl
c 254	10.8	37.2	25	6	AB575576	Ab575576 Human PAP	c 327	10.8	37.2	65	6	ABN56758	Abn56758 Mouse spl
c 255	10.8	37.2	25	6	AB575574	Ab575574 Human PAP	c 328	10.6	36.6	23	2	AA101534	Aat01534 Human her
c 256	10.8	37.2	25	6	AB575575	Ab575575 Human PAP	c 329	10.6	36.6	23	2	AA101534	Aat01534 Human her
c 257	10.8	37.2	25	8	ACK80900	Ack80900 Human mic	c 330	10.6	36.6	24	3	AAZ35966	Aaz35966 Cytochrom
c 258	10.8	37.2	25	8	AC165128	Ac165128 Human mic	c 331	10.6	36.6	24	3	ABT31746	Abt31746 IRF1 p53
c 259	10.8	37.2	25	8	AC153509	Ac153509 Human mic	c 332	10.6	36.6	25	8	AC171263	Ac171263 Human mic
c 260	10.8	37.2	25	8	ACK38091	Ack38091 Human mic	c 333	10.6	36.6	25	8	AC132666	Ac132666 Human mic
c 261	10.8	37.2	25	8	ACH52985	Ach52985 DNA targe	c 334	10.6	36.6	25	8	AC195082	Ac195082 Human mic
c 262	10.8	37.2	27	4	AAZ27163	Aaz27163 Caenorhab	c 335	10.6	36.6	25	8	ACK06797	Ack06797 Human mic
c 263	10.8	37.2	27	4	AAH38439	Aah38439 SNP speci	c 336	10.6	36.6	25	8	AC101290	Ac101290 Human mic
c 264	10.8	37.2	29	3	AAA42116	Aaa42116 Polymorph	c 337	10.6	36.6	25	8	AC101291	Ac101291 Human mic
c 265	10.8	37.2	29	3	AAAI0646	Aaa10646 PCR prime	c 338	10.6	36.6	28	3	AAA40375	Aaa40375 Feline fo
c 266	10.8	37.2	30	9	ADC65106	Adc65106 Primer #1	c 339	10.6	36.6	29	2	AAQ43929	Aaa43929 Primer BL
c 267	10.8	37.2	32	9	ADC58048	Adc58048 PCR prime	c 340	10.6	36.6	29	3	AAA04444	Aaa04444 Polymorph
c 268	10.8	37.2	33	6	ABL54520	Ab154520 Pectinatu	c 341	10.6	36.6	29	7	ACC59203	Acc59203 Human ade
c 269	10.8	37.2	33	7	ACC00085	Acc00085 Primer #4	c 342	10.6	36.6	29	7	ACC59205	Acc59205 Human ade
c 270	10.8	37.2	33	9	ADB9297	Adb9297 PCR prime	c 343	10.6	36.6	30	2	RAY28008	Ray28008 E3L RNA b
c 271	10.8	37.2	35	2	AAZ99670	Aaz99670 Reverse p	c 344	10.6	36.6	30	2	AAZ30456	Aaz30456 Primer 9
c 272	10.8	37.2	40	3	AAAS1108	Aaa51108 Oligomer	c 345	10.6	36.6	30	4	ABX89507	Abx89507 Soybean p
c 273	10.8	37.2	40	6	ABL54532	Ab154532 Pectinatu	c 346	10.6	36.6	30	6	ABX69591	Abx69591 Novel Hel
c 274	10.8	37.2	40	6	ABK83286	Abk83286 Human ser	c 347	10.6	36.6	30	9	ADB85428	Adb85428 PCR prime
c 275	10.8	37.2	41	3	AAAY70544	Aaa70544 Reverse p	c 348	10.6	36.6	31	4	ABL48203	Ab148203 Human GRI
c 276	10.8	37.2	41	6	ABZ48930	Abz48930 Human ald	c 349	10.6	36.6	31	4	ABL48019	Ab148019 Human GRI
c 277	10.8	37.2	41	6	ABZ46418	Abz46418 Human ald	c 350	10.6	36.6	31	4	ABL48014	Ab148014 Human GRI
c 278	10.8	37.2	42	6	ABK93317	Abk93317 Human 5-h	c 351	10.6	36.6	31	6	ABK21667	Abk21667 Human ERG
c 279	10.8	37.2	43	6	ABZ27920	Abz27920 Candida e	c 352	10.6	36.6	31	6	ABK21707	Abk21707 Human ERG
c 280	10.8	37.2	45	2	AAQ69592	Aaq69592 Human gen	c 353	10.6	36.6	31	6	ABK21754	Abk21754 Human ERG
c 281	10.8	37.2	45	2	AAQ69380	Aaq69380 Human fib	c 354	10.6	36.6	31	6	ABK21513	Abk21513 Human ERG
c 282	10.8	37.2	45	2	AAQ64054	Aat64054 Human fib	c 355	10.6	36.6	31	6	ABK60174	Abk60174 Human CLC
c 283	10.8	37.2	45	2	AAT63842	Aat63842 Human fib	c 356	10.6	36.6	31	6	ABK59880	Abk59880 Human CLC
c 284	10.8	37.2	45	2	AAI17130	Aai17130 Test sequ	c 357	10.6	36.6	31	6	ABK60180	Abk60180 Human CLC
c 285	10.8	37.2	45	2	AAI17342	Aai17342 Test sequ	c 358	10.6	36.6	31	6	ABK59976	Abk59976 Human CLC
c 286	10.8	37.2	45	6	ABK82833	Abk82833 DNA bindi	c 359	10.6	36.6	31	6	ABK60209	Abk60209 Human CLC
c 287	10.8	37.2	45	6	ABK92621	Abk92621 DNA bindi	c 360	10.6	36.6	31	7	ACA08645	Acca08645 Necrosia
c 288	10.8	37.2	45	9	ABK32438	Abk32438 Rat p60TR	c 361	10.6	36.6	31	7	ABZ66333	Abz66333 Human HER
c 289	10.8	37.2	45	10	ADB80160	Adb80160 Duplex ol	c 362	10.6	36.6	31	7	ABZ66068	Abz66068 Human HER
c 290	10.8	37.2	45	10	ADB80372	Adb80372 Duplex ol	c 363	10.6	36.6	31	7	ABZ65632	Abz65632 Human HER
c 291	10.8	37.2	47	3	AAZ87939	Aaz87939 Human map	c 364	10.6	36.6	31	7	ABZ65797	Abz65797 Human HER
c 292	10.8	37.2	48	2	AAI02929	Aai02929 Human glu	c 365	10.6	36.6	31	7	ABZ65906	Abz65906 Human H-R
c 293	10.8	37.2	50	2	AAQ69593	Aaq69593 Human gen	c 366	10.6	36.6	31	7	ABZ62376	Abz62376 Human K-R
c 294	10.8	37.2	50	2	AAT64055	Aat64055 Human gen	c 367	10.6	36.6	31	7	ABZ64179	Abz64179 Human H-R
c 295	10.8	37.2	50	2	AAI17343	Aai17343 Test sequ	c 368	10.6	36.6	31	7	ABZ66071	Abz66071 Human HER
c 296	10.8	37.2	50	3	AAAS1146	Aaa51146 Oligomer	c 369	10.6	36.6	31	7	ACD62205	Accd62205 HCV minus
c 297	10.8	37.2	50	3	AAZ29462	Aaz29462 PCR prime	c 370	10.6	36.6	31	7	ACD59882	Accd59882 HCV DNazy
c 298	10.8	37.2	50	4	AAI128930	Aai128930 Human SNP	c 371	10.6	36.6	31	7	ACD61654	Accd61654 HCV minus
c 299	10.8	37.2	50	6	ABK82834	Abk82834 DNA bindi	c 372	10.6	36.6	31	7	ACD58557	Accd58557 HCV DNazy
c 300	10.8	37.2	50	6	ABZ01498	Abz01498 Human leu	c 373	10.6	36.6	31	7	ACD57211	Accd57211 HCV DNazy
c 301	10.8	37.2	50	6	ABZ00126	Abz00126 Human leu	c 374	10.6	36.6	31	7	ACD59572	Accd59572 HCV minus
c 302	10.8	37.2	50	6	ABZ03691	Abz03691 Human leu	c 375	10.6	36.6	31	7	ACD65339	Accd65339 HCV minus
c 303	10.8	37.2	50	6	ABZ02255	Abz02255 Human leu	c 376	10.6	36.6	31	7	ACD62869	Accd62869 HCV minus
c 304	10.8	37.2	50	10	ADB80373	Adb80373 Duplex ol	c 377	10.6	36.6	31	7	ACD54958	Accd54958 HCV DNazy
c 305	10.8	37.2	51	4	AAI126990	Aai126990 Human SNP	c 378	10.6	36.6	31	7	ACD60482	Accd60482 HCV DNazy
c 306	10.8	37.2	51	4	AAH90685	Aah90685 Human CLO	c 379	10.6	36.6	33	6	ABK14720	Abk14720 Pogo conv
c 307	10.8	37.2	51	4	AAH39728	Aah39728 Human SNP	c 380	10.6	36.6	33	6	AAI47565	Aai47565 Human pur
c 308	10.8	37.2	51	4	AAH40360	Aah40360 Human SNP	c 381	10.6	36.6	33	6	ABL55338	Ab155338 Human RNA
c 309	10.8	37.2	51	6	AB198852	Ab198852 Oligonucl	c 382	10.6	36.6	34	9	ADC40550	Adc40550 Replicati
c 310	10.8	37.2	60	6	ABN50311	Abn50311 Human spl	c 383	10.6	36.6	35	4	AAI13700	Aai13700 Arabidops
c 311	10.8	37.2	60	6	ABN42592	Abn42592 Human spl	c 384	10.6	36.6	38	2	AAV07069	Aav07069 Degenerat
c 312	10.8	37.2	60	6	ABN59107	Abn59107 Human spl	c 385	10.6	36.6	39	7	ABX99212	Abx99212 Human CAN
c 313	10.8	37.2	60	6	ABN47524	Abn47524 Human spl	c 386	10.6	36.6	40	7	ABZ72385	Abz72385 Tomato.sp
c 314	10.8	37.2	60	6	ABN41771	Abn41771 Human spl	c 387	10.6	36.6	41	2	AAQ89859	Aaq89859 PUC 525 p
c 315	10.8	37.2	60	6	ABN45568	Abn45568 Human spl	c 388	10.6	36.6	41	6	ABV72968	Abv72968 Human PWM

C 389	10.6	36.6	41	6	ABZ50144	Abz50144 Human NDU	462	10.4	35.9	25	8	ACI49963	Human mic
C 390	10.6	36.6	41	6	ABZ44134	Abz44134 Human NDU	463	10.4	35.9	26	2	AAT71933	Primer de
C 391	10.6	36.6	43	6	ABL51319	AbL51319 Bacteriop	464	10.4	35.9	26	2	AAT72005	Primer de
C 392	10.6	36.6	43	6	ABL51317	AbL51317 Bacteriop	465	10.4	35.9	27	3	AAZ32859	Laccococc
C 393	10.6	36.6	47	3	AZ67926	Az67926 Human map	466	10.4	35.9	27	5	AAZ09842	Primer fo
C 394	10.6	36.6	50	6	AZ200247	Az200247 Human leu	467	10.4	35.9	27	6	ABN85152	Abn85152 HIV gp41
C 395	10.6	36.6	50	6	AZ2001788	Az2001788 Human leu	468	10.4	35.9	27	6	ABN85151	Abn85151 HIV gp41
C 396	10.6	36.6	50	6	AZ2002061	Az2002061 Human leu	469	10.4	35.9	29	2	AAT97220	Immunoglo
C 397	10.6	36.6	50	6	AZ206279	Az206279 Human leu	470	10.4	35.9	29	2	ABK87921	PCR prime
C 398	10.6	36.6	50	6	AZ204324	Az204324 Human leu	471	10.4	35.9	30	4	AH43281	D-aminac
C 399	10.6	36.6	51	2	AAL28434	Aal28434 Human SNP	472	10.4	35.9	31	2	AAV67928	Nucleotid
C 400	10.6	36.6	52	4	AA79606	Aa79606 Capture e	473	10.4	35.9	31	3	AAA79150	Human gen
C 401	10.6	36.6	53	7	ABX54825	Abx54825 Bovine ES	474	10.4	35.9	31	3	AAA78689	Human gen
C 402	10.6	36.6	54	2	AAT43638	Aat43638 HIV-1 mat	475	10.4	35.9	33	6	ABA02362	Human nuc
C 403	10.6	36.6	54	2	AAQ68886	AaQ68886 VDJ junct	476	10.4	35.9	33	7	ABZ57688	Transcrip
C 404	10.6	36.6	60	6	ABN35687	Abn35687 Human spl	477	10.4	35.9	33	9	ADZ76704	Staphyloc
C 405	10.6	36.6	60	6	ABN39064	Abn39064 Human spl	478	10.4	35.9	36	1	AAH10057	Sequence
C 406	10.6	36.6	60	6	ABN47161	Abn47161 Human spl	479	10.4	35.9	36	6	ABZ71073	Plasmid p
C 407	10.6	36.6	60	6	ABN33758	Abn33758 Human spl	480	10.4	35.9	36	6	ABZ71074	Plasmid p
C 408	10.6	36.6	60	6	ABN46195	Abn46195 Human spl	481	10.4	35.9	36	6	ABS66491	Bacteriop
C 409	10.6	36.6	60	6	ABN49699	Abn49699 Human spl	482	10.4	35.9	36	6	ABS66490	Bacteriop
C 410	10.6	36.6	60	6	ABN47267	Abn47267 Human spl	483	10.4	35.9	36	9	ADD24253	Prion dis
C 411	10.6	36.6	60	6	ABN33531	Abn33531 Human spl	484	10.4	35.9	36	9	ADD24252	Prion dis
C 412	10.6	36.6	60	6	ABN47600	Abn47600 Human spl	485	10.4	35.9	37	7	ACC70115	Nucleotid
C 413	10.6	36.6	60	6	ABN33172	Abn33172 Human spl	486	10.4	35.9	38	6	ABK21095	Human ERG
C 414	10.6	36.6	60	6	ABN44580	Abn44580 Human spl	487	10.4	35.9	38	6	ACD53775	HBV zinzy
C 415	10.6	36.6	60	6	ABN43229	Abn43229 Human spl	488	10.4	35.9	39	9	ADZ87739	Human neu
C 416	10.6	36.6	60	6	ABN41377	Abn41377 Human spl	489	10.4	35.9	40	2	AAZ03169	Aax03169 RSVB poly
C 417	10.6	36.6	60	7	ACC44953	Acc44953 Candida u	490	10.4	35.9	40	2	ABN84179	Primer HM
C 418	10.6	36.6	63	4	AAZ32287	Aaz32287 GAP repal	491	10.4	35.9	41	2	AAV51170	Maize pol
C 419	10.6	36.6	64	4	AAK96512	Aak96512 Human neu	492	10.4	35.9	41	2	AAV61543	Primer, u
C 420	10.6	36.6	64	4	AAK98005	Aak98005 Human neu	493	10.4	35.9	41	2	AAV33319	Anti-CD23
C 421	10.6	36.6	64	4	ABT01282	Abt01282 Human neu	494	10.4	35.9	41	6	ABZ50480	Human ary
C 422	10.6	36.6	64	6	ABT02775	Abt02775 Human neu	495	10.4	35.9	41	6	ABZ44491	Human ary
C 423	10.6	36.6	65	6	ABZ29669	Abz29669 Candida g	496	10.4	35.9	41	7	ABZ25086	MEN2 rela
C 424	10.6	36.6	65	6	ABZ28932	Abz28932 Candida g	497	10.4	35.9	42	9	ADD14852	U. maydis
C 425	10.6	36.6	65	6	ABN29378	Abn29378 Rat splic	498	10.4	35.9	43	6	ABZ27007	Candida e
C 426	10.6	36.6	65	6	ABN53008	Abn53008 Mouse spl	499	10.4	35.9	43	3	AAZ65786	Human map
C 427	10.6	36.6	65	6	ABN53393	Abn53393 Mouse spl	500	10.4	35.9	47	3	AAZ66387	Human map
C 428	10.6	36.6	65	6	ABN51562	Abn51562 Mouse spl	501	10.4	35.9	47	3	AAZ68544	Human map
C 429	10.6	36.6	66	8	AAI62774	Aai62774 Escherich	502	10.4	35.9	47	3	AAZ68321	Human map
C 430	10.6	36.6	69	2	AAV30083	Aav30083 Probe use	503	10.4	35.9	47	6	ABK40908	Human map
C 431	10.6	36.6	69	4	AAZ21265	Aaz21265 Interleuk	504	10.4	35.9	47	6	ABK40908	Human obe
C 432	10.6	36.6	69	4	ABX96959	Abx96959 Interleuk	505	10.4	35.9	50	3	AAAG9485	EMP-Fc fu
C 433	10.6	36.6	69	8	ABX80098	Abx80098 Cytokine	506	10.4	35.9	50	3	AAAC22564	Human sec
C 434	10.6	36.6	70	3	ABK027314	Abk027314 Human sec	507	10.4	35.9	50	6	ABZ35727	BPO mimet
C 435	10.4	35.9	17	4	ABK02859	Abk02859 Human CD2	508	10.4	35.9	50	6	AAZ0794	Clostridi
C 436	10.4	35.9	17	4	ABK03226	Abk03226 Human CD2	509	10.4	35.9	50	6	AAZ0795	Clostridi
C 437	10.4	35.9	17	4	ABK03604	Abk03604 Human CD2	510	10.4	35.9	50	6	AAZ0795	Clostridi
C 438	10.4	35.9	17	6	ABK92373	Abk92373 Human GST	511	10.4	35.9	50	6	ABZ05502	Human leu
C 439	10.4	35.9	17	7	ACD50561	Acd50561 HBV hamme	512	10.4	35.9	50	6	ABZ02633	Human leu
C 440	10.4	35.9	17	7	ACD51988	Acd51988 HBV inozy	513	10.4	35.9	51	4	AAZ27201	Human SNP
C 441	10.4	35.9	17	7	ACD50560	Acd50560 HBV hamme	514	10.4	35.9	51	4	AAZ2743	Human SNP
C 442	10.4	35.9	18	4	AAZ02018	Aaz02018 PCR prime	515	10.4	35.9	51	4	AAZ29742	Human SNP
C 443	10.4	35.9	20	2	AAZ05960	Aaz05960 PCR prime	516	10.4	35.9	51	4	AAZ33702	Human SNP
C 444	10.4	35.9	20	3	AAZ71201	Aaz71201 Human bia	517	10.4	35.9	51	4	AAI78961	Human spl
C 445	10.4	35.9	20	4	AAZ30814	Aaz30814 Human cer	518	10.4	35.9	51	4	AAI75310	Human sil
C 446	10.4	35.9	20	7	AAZ54521	Aaz54521 BACZRA PC	519	10.4	35.9	51	4	AAI75310	Human sil
C 447	10.4	35.9	20	7	AAZ44040	Aaz44040 Oligo ISI	520	10.4	35.9	52	2	AAV44499	Biotinyl
C 448	10.4	35.9	21	2	AAZ28450	Aaz28450 Target ga	521	10.4	35.9	52	2	AAV44499	Biotinyl
C 449	10.4	35.9	21	2	AAV67325	Aav67325 Nucleotid	522	10.4	35.9	57	3	AAAG9485	EMP-BMP-F
C 450	10.4	35.9	22	2	AAV51576	Aav51576 Zea mays	523	10.4	35.9	57	6	AAZ35739	Lac promc
C 451	10.4	35.9	24	6	ABQ02189	Abq02189 Oligonuc1	524	10.4	35.9	59	3	AAI7294	Human sec
C 452	10.4	35.9	24	9	ADZ64604	Adz64604 Somatosta	525	10.4	35.9	59	6	AAZ47051	Human bet
C 453	10.4	35.9	25	8	ACI66117	AcI66117 Human mic	526	10.4	35.9	60	3	AAAG9485	EMP-BMP-F
C 454	10.4	35.9	25	8	ACI12818	AcI12818 Human mic	527	10.4	35.9	60	6	ABN37841	Human spl
C 455	10.4	35.9	25	8	ACI49962	AcI49962 Human mic	528	10.4	35.9	60	6	ABN37841	Human spl
C 456	10.4	35.9	25	8	ACI23806	AcI23806 Human mic	529	10.4	35.9	60	6	ABN37841	Human spl
C 457	10.4	35.9	25	8	ACI110053	AcI110053 Human mic	530	10.4	35.9	60	6	ABN37841	Human spl
C 458	10.4	35.9	25	8	ACI110052	AcI110052 Human mic	531	10.4	35.9	60	6	ABN37841	Human spl
C 459	10.4	35.9	25	8	ACI22819	AcI22819 Human mic	532	10.4	35.9	60	6	ABN37841	Human spl
C 460	10.4	35.9	25	8	ACI22819	AcI22819 Human mic	533	10.4	35.9	60	6	ABN37841	Human spl
C 461	10.4	35.9	25	8	ACI22819	AcI22819 Human mic	534	10.4	35.9	60	6	ABN37841	Human spl

535	10.4	35.9	60	6	ABN40128	Human spl
536	10.4	35.9	60	6	ABN43390	Human spl
537	10.4	35.9	60	6	ABN49374	Human spl
538	10.4	35.9	60	6	ABN49153	Human spl
539	10.4	35.9	61	3	AA69484	EMF-Pc fu
540	10.4	35.9	61	6	ABL35726	EPO minet
541	10.4	35.9	64	9	ADC64605	Somatosta
542	10.4	35.9	65	6	ABN28812	Rat splic
543	10.4	35.9	65	6	ABN54938	Mouse spl
544	10.4	35.9	66	9	ADC64602	Somatosta
545	10.4	35.9	67	3	AAC32336	Human sec
546	10.4	35.9	67	3	ADC64612	Somatosta
547	10.4	35.9	70	5	AAF29244	Ligand to
548	10.4	35.9	71	2	AAT65354	Human ker
549	10.4	35.9	77	1	AAAN92360	Gene for
550	10.4	35.9	77	2	AAQ03553	DNA seque
551	10.4	35.9	79	1	AAAN81448	New DNA s
552	10.4	35.9	79	1	AAAN80972	Synthetic
553	10.4	35.9	79	1	AAAN81355	Sequence
554	10.4	35.9	79	1	AAAN81283	Sequence
555	10.2	35.2	20	4	AAH45015	PCR prime
556	10.2	35.2	20	6	ABT13913	Human hel
557	10.2	35.2	20	6	ABT06452	RARbeta2
558	10.2	35.2	20	6	ABI92997	Capture o
559	10.2	35.2	21	3	ADC66135	Human CFT
560	10.2	35.2	21	3	AZ77352	Human bia
561	10.2	35.2	21	6	ABS97827	Human NAD
562	10.2	35.2	21	6	ABS97828	Human NAD
563	10.2	35.2	22	2	AAQ21481	CTP synth
564	10.2	35.2	22	2	AAT47391	Primer #1
565	10.2	35.2	22	6	ABS71777	Human rev
566	10.2	35.2	23	2	AAT66337	5' primer
567	10.2	35.2	23	6	ABS63220	Identific
568	10.2	35.2	23	6	ABL56402	PCR prime
569	10.2	35.2	23	6	ABL56399	PCR prime
570	10.2	35.2	23	6	ABL56396	PCR prime
571	10.2	35.2	24	3	ABE14269	Optineuri
572	10.2	35.2	24	4	AAF79515	Human G p
573	10.2	35.2	24	6	ABQ93701	Minimally
574	10.2	35.2	24	6	ADQ26967	BHI PCR p
575	10.2	35.2	24	6	ASQ05709	Oligonucl
576	10.2	35.2	24	6	ABQ05750	Oligonucl
577	10.2	35.2	24	6	ABQ00872	Oligonucl
578	10.2	35.2	24	6	AAI44308	Human phy
579	10.2	35.2	24	6	ABL49629	Human G p
580	10.2	35.2	24	6	ABI86444	Capture o
581	10.2	35.2	24	6	ABI88301	Capture o
582	10.2	35.2	24	6	ABI90989	Capture o
583	10.2	35.2	24	6	ABI86445	Capture o
584	10.2	35.2	24	6	ABI84723	Capture o
585	10.2	35.2	24	6	ABI90988	Capture o
586	10.2	35.2	24	6	ABI84722	Capture o
587	10.2	35.2	24	6	ABI88300	Capture o
588	10.2	35.2	24	7	ABZ70877	Human mal
589	10.2	35.2	24	8	ADA38214	Reverse P
590	10.2	35.2	24	9	ADC66118	Human CFT
591	10.2	35.2	24	9	ADD69100	Angiogene
592	10.2	35.2	25	3	AAA68557	Bacteriop
593	10.2	35.2	25	6	ABK97984	Cell-TRAP
594	10.2	35.2	25	7	ABZ23287	PCR prime
595	10.2	35.2	25	8	ACT107607	Human mic
596	10.2	35.2	25	8	ACK17919	Human mic
597	10.2	35.2	25	8	ACI59738	Human mic
598	10.2	35.2	25	8	ACI61052	Human mic
599	10.2	35.2	25	8	ACK27961	Human mic
600	10.2	35.2	25	8	ACT07606	Human mic
601	10					

C 681	10.2	35.2	46	2	AAV48399	Aav48399 P. damsel	C 754	10.2	35.2	60	6	ABN46973	Abn46973 Human spl
C 682	10.2	35.2	46	2	AAV33359	Aav33359 Primer BS	755	10.2	35.2	60	6	ABN32898	Abn32898 Human spl
C 683	10.2	35.2	46	2	AAV58401	Aav58401 Primer BS	756	10.2	35.2	60	6	ABN42766	Abn42766 Human spl
C 684	10.2	35.2	46	3	AAV57661	Aav57661 PCR prime	C 757	10.2	35.2	60	6	ABN46832	Abn46832 Human spl
C 685	10.2	35.2	47	2	AAV303527	Aav303527 Fragment	758	10.2	35.2	60	6	ABN49200	Abn49200 Human spl
C 686	10.2	35.2	47	3	AAV289012	Aav289012 Human map	759	10.2	35.2	60	6	ABN33787	Abn33787 Human spl
C 687	10.2	35.2	47	3	AAV286662	Aav286662 Human map	760	10.2	35.2	60	6	ABN38791	Abn38791 Human spl
C 688	10.2	35.2	47	3	AAV286629	Aav286629 Human map	761	10.2	35.2	60	6	ABN36323	Abn36323 Human spl
C 689	10.2	35.2	47	3	AAV2868609	Aav2868609 Human map	762	10.2	35.2	60	6	ABN42576	Abn42576 Human spl
C 690	10.2	35.2	47	3	AAV266750	Aav266750 Human map	763	10.2	35.2	60	6	ABN41092	Abn41092 Human spl
C 691	10.2	35.2	48	2	AAV69441	Aav69441 Human int	764	10.2	35.2	60	6	ABN58792	Abn58792 Human spl
C 692	10.2	35.2	48	2	AAV63903	Aav63903 Human int	765	10.2	35.2	60	6	ABN39736	Abn39736 Human spl
C 693	10.2	35.2	48	2	AAV17191	Aav17191 Test sequ	766	10.2	35.2	60	6	ABN49094	Abn49094 Human spl
C 694	10.2	35.2	48	6	ABK82682	Abk82682 DNA bindi	C 767	10.2	35.2	60	9	ABN87528	Abn87528 Bovine la
C 695	10.2	35.2	48	10	ABE80221	Abe80221 Duplex ol	C 768	10.2	35.2	63	2	AAQ14150	Aaq14150 Probe f63
C 696	10.2	35.2	49	2	AAAT80446	Aat80446 Hepatoma	C 769	10.2	35.2	64	2	AAQ14150	Aaq14150 Ribozyme
C 697	10.2	35.2	50	1	AAAN91943	Aan91943 Complement	C 770	10.2	35.2	64	3	AAZ50738	Aaz50738 Human gen
C 698	10.2	35.2	50	2	AAQ35511	Aaq35511 C7L-KIL d	C 771	10.2	35.2	65	2	AAV70297	Aav70297 Murine os
C 699	10.2	35.2	50	2	AAQ69716	Aaq69716 Human leu	C 772	10.2	35.2	65	2	AAV30440	Aav30440 3' primer
C 700	10.2	35.2	50	2	AAV43989	Aav43989 Octopline	773	10.2	35.2	65	2	AAV30440	Aav30440 3' primer
C 701	10.2	35.2	50	2	AAV64178	Aav64178 Human leu	C 774	10.2	35.2	65	2	ABZ28536	Abz28536 Candida g
C 702	10.2	35.2	50	2	AAV15878	Aav15878 nos promo	C 775	10.2	35.2	65	6	ABZ28536	Abz28536 Candida g
C 703	10.2	35.2	50	2	AAV64331	Aav64331 NOS promo	C 776	10.2	35.2	65	6	ABN28787	Abn28787 Rat splic
C 704	10.2	35.2	50	2	AAV17466	Aav17466 Test sequ	C 777	10.2	35.2	65	6	ABN55103	Abn55103 Mouse spl
C 705	10.2	35.2	50	4	AAAL33910	Aal33910 Human SNP	C 778	10.2	35.2	65	6	ABN55401	Abn55401 Mouse spl
C 706	10.2	35.2	50	4	AAAL30363	Aal30363 Human SNP	C 779	10.2	35.2	65	6	ABN58324	Abn58324 Mouse spl
C 707	10.2	35.2	50	4	AAAL30364	Aal30364 Human SNP	C 780	10.2	35.2	65	6	ABN30797	Abn30797 Rat splic
C 708	10.2	35.2	50	4	AAAL34625	Aal34625 Human SNP	C 781	10.2	35.2	65	6	ABN28242	Abn28242 Rat splic
C 709	10.2	35.2	50	6	ABK82957	Abk82957 DNA bindi	C 782	10.2	35.2	65	6	ABN31227	Abn31227 Rat splic
C 710	10.2	35.2	50	6	ABK82957	Abk82957 DNA bindi	C 783	10.2	35.2	65	6	ABN53839	Abn53839 Mouse spl
C 711	10.2	35.2	50	6	ABZ01018	Abz01018 Human leu	C 784	10.2	35.2	65	6	ABN54772	Abn54772 Mouse spl
C 712	10.2	35.2	50	6	ABZ04420	Abz04420 Human leu	C 785	10.2	35.2	65	6	ABN51484	Abn51484 Mouse spl
C 713	10.2	35.2	50	6	ABZ01807	Abz01807 Human leu	C 786	10.2	35.2	65	6	ABN27984	Abn27984 Rat splic
C 714	10.2	35.2	50	6	ABZ05309	Abz05309 Human leu	C 787	10.2	35.2	65	6	ABN29876	Abn29876 Rat splic
C 715	10.2	35.2	50	6	ABZ05216	Abz05216 Human leu	C 788	10.2	35.2	65	6	ABN29876	Abn29876 Rat splic
C 716	10.2	35.2	50	6	ABZ00318	Abz00318 Human leu	C 789	10.2	35.2	65	6	ABN56497	Abn56497 Mouse spl
C 717	10.2	35.2	50	6	ABZ01662	Abz01662 Human leu	790	10.2	35.2	65	6	ABN57693	Abn57693 Mouse spl
C 718	10.2	35.2	50	6	ABZ02573	Abz02573 Human leu	C 791	10.2	35.2	65	6	ABN30287	Abn30287 Rat splic
C 719	10.2	35.2	50	10	ADE80496	Ade80496 Duplex ol	C 792	10.2	35.2	65	6	ABN52191	Abn52191 Mouse spl
C 720	10.2	35.2	51	3	AAV76623	Aav76623 Human clo	793	10.2	35.2	65	6	ABN28517	Abn28517 Rat splic
C 721	10.2	35.2	51	4	AAAL34009	Aal34009 Human SNP	C 794	10.2	35.2	65	6	ABN55469	Abn55469 Mouse spl
C 722	10.2	35.2	51	4	AAAL27454	Aal27454 Human SNP	795	10.2	35.2	65	6	ABN55379	Abn55379 Mouse spl
C 723	10.2	35.2	51	4	AAAL32109	Aal32109 Human SNP	C 796	10.2	35.2	66	2	AAV77042	Aav77042 Staphyloc
C 724	10.2	35.2	51	4	AAAL31162	Aal31162 Human SNP	C 797	10.2	35.2	66	5	AAAS43745	Aas43745 Corneodes
C 725	10.2	35.2	51	4	AAAL29578	Aal29578 Human SNP	C 798	10.2	35.2	66	3	ABQ75624	Abq75624 Human SEB
C 726	10.2	35.2	51	4	AAAL28379	Aal28379 Human SNP	C 799	10.2	35.2	68	3	AAQ35849	Aaq35849 T1, T2, T
C 727	10.2	35.2	51	4	AAH74294	Aah74294 Human sil	800	10.2	35.2	70	2	AAQ35849	Aaq35849 PCR prime
C 728	10.2	35.2	51	4	AAH90333	Aah90333 Human clo	801	10.2	35.2	70	2	AAQ35849	Aaq35849 PCR prime
C 729	10.2	35.2	51	4	AAH89568	Aah89568 Human ATP	802	10.2	35.2	70	2	AAQ35849	Aaq35849 PCR prime
C 730	10.2	35.2	51	4	AAH89570	Aah89570 Human ATP	C 803	10.2	35.2	71	2	AAAT78751	Aat78751 L-selecti
C 731	10.2	35.2	51	4	AAH37244	Aah37244 Human SNP	C 804	10.2	35.2	71	8	ADA21838	Ada21838 HGF 30N8
C 732	10.2	35.2	51	4	AAH38440	Aah38440 Human SNP	C 805	10.2	35.2	74	4	AAH71988	Aah71988 Human cer
C 733	10.2	35.2	51	4	AAH40176	Aah40176 Human SNP	C 806	10.2	35.2	79	4	AAK55455	Aak55455 Human inm
C 734	10.2	35.2	51	4	AAH79827	Aah79827 Human DNA	C 807	10.2	35.2	80	6	ACC60524	Acc60524 Polynucle
C 735	10.2	35.2	51	4	AAH29247	Aah29247 Human DNA	C 808	10.2	35.2	80	6	ACC60527	Acc60527 Polynucle
C 736	10.2	35.2	56	2	AAZ22478	Aaz22478 Oligonuc	C 809	10.2	35.2	80	6	ABT05406	Abt05406 Human ant
C 737	10.2	35.2	59	2	AAV70298	Aav70298 Murine os	C 810	10.2	35.2	16	6	ABK46946	Abk46946 COX-2 ant
C 738	10.2	35.2	59	7	ABE80105	Abe80105 Cuphea pu	811	10	34.5	17	4	ABA77841	Aba77841 BRCA1 mut
C 739	10.2	35.2	59	7	ABE80099	Abe80099 Cuphea pu	812	10	34.5	17	4	ABA77841	Aba77841 BRCA1 mut
C 740	10.2	35.2	60	6	ABK97330	Abk97330 RNA for G	C 813	10	34.5	17	4	ABA77834	Aba77834 BRCA1 mut
C 741	10.2	35.2	60	6	ABK32977	Abk32977 Homologou	C 814	10	34.5	17	4	ABA77834	Aba77834 BRCA1 mut
C 742	10.2	35.2	60	6	ABN46509	Abn46509 Human spl	C 815	10	34.5	17	4	ABA77834	Aba77834 BRCA1 mut
C 743	10.2	35.2	60	6	ABN37807	Abn37807 Human spl	C 816	10	34.5	17	4	ABA77834	Aba77834 BRCA1 mut
C 744	10.2	35.2	60	6	ABN35977	Abn35977 Human spl	C 817	10	34.5	17	4	ABA77834	Aba77834 BRCA1 mut
C 745	10.2	35.2	60	6	ABN44005	Abn44005 Human spl	C 818	10	34.5	17	7	ACC63412	Acc63412 HCV minus
C 746	10.2	35.2	60	6	ABN48250	Abn48250 Human spl	C 819	10	34.5	17	9	ADB42954	Adb42954 Tumour su
C 747	10.2	35.2	60	6	ABN37007	Abn37007 Human spl	C 820	10	34.5	17	9	ADB42954	Adb42954 Tumour su
C 748	10.2	35.2	60	6	ABN41524	Abn41524 Human spl	C 821	10	34.5	19	3	AAZ71864	Aaz71864 Human bia
C 749	10.2	35.2	60	6	ABN41524	Abn41524 Human spl	C 822	10	34.5	20	2	AAQ37996	Aaq37996 Peptide n
C 750	10.2	35.2	60	6	ABN47597	Abn47597 Human spl	C 823	10	34.5	20	2	AAQ37996	Aaq37996 Peptide n
C 751	10.2	35.2	60	6	ABN36497	Abn36497 Human spl	C 824	10	34.5	20	2	AAQ37996	Aaq37996 Peptide n
C 752	10.2	35.2	60	6	ABN43599	Abn43599 Human spl	C 825	10	34.5	20	2	AAQ37996	Aaq37996 Peptide n
C 753	10.2	35.2	60	6	ABN43599	Abn43599 Human spl	C 826	10	34.5	20	2	AAQ37996	Aaq37996 Peptide n

C 973 10 34.5 31 6 ABK59591 Human CLC
C 974 10 34.5 31 6 ABK60175 Human CLC
C 975 10 34.5 31 6 ABK60218 Human CLC
C 976 10 34.5 31 7 ACA08736 Necrosis
C 977 10 34.5 31 7 ACA08357 Necrosis
C 978 10 34.5 31 7 ACA08519 Necrosis
C 979 10 34.5 31 7 ACA08428 Necrosis
C 980 10 34.5 31 7 ABZ64323 Human H-R
C 981 10 34.5 31 7 ABZ65625 Human HER
C 982 10 34.5 31 7 ABZ66411 Human HER
C 983 10 34.5 31 7 ABZ66193 Human HER
C 984 10 34.5 31 7 ABZ63649 Human H-R
C 985 10 34.5 31 7 ABZ65802 Human HER
C 986 10 34.5 31 7 ABZ66429 Human HER
C 987 10 34.5 31 7 ABZ63855 Human H-R
C 988 10 34.5 31 7 ABZ65950 Human HER
C 989 10 34.5 31 7 ABZ66027 Human HER
C 990 10 34.5 31 7 ABZ64429 Human H-R
C 991 10 34.5 31 7 ABZ64440 Human H-R
C 992 10 34.5 31 7 ABZ66392 Human HER
C 993 10 34.5 31 7 ABZ62244 Human K-R
C 994 10 34.5 31 7 ABZ63310 Human K-R
C 995 10 34.5 31 7 ABZ66208 Human HER
C 996 10 34.5 31 7 ABZ66420 Human HER
C 997 10 34.5 31 7 ABZ62308 Human K-R
C 998 10 34.5 31 7 ABZ63853 Human H-R
C 999 10 34.5 31 7 ABZ65850 Human HER
C 1000 10 34.5 31 7 ABZ65732 Human HER

ALIGNMENTS

RESULT 1
ID AAA70827 standard; RNA; 29 BP.
XX AC
XX AAA70827;
XX 27-APR-2001 (first entry)
XX Molecular interaction site RNA #27.
XX Modulator; identification; molecular interaction; virtual library; ss.
XX Synthetic.
XX WO9558947-A2.
XX 18-NOV-1999.
XX 12-MAY-1999; 99WO-US010361.
XX 12-MAY-1998; 98US-00076404.
XX 12-MAY-1998; 98US-0085092P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX Claim 235; Page 235; 405pp; English.

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of

CC the target RNA; (b) generating in silico a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified and isolated RNA fragment comprising the human sequence UUUACAAUAUACUAGUACAGAAAAAUC (11). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds

XX Sequence 29 BP; 4 A; 4 C; 5 G; 0 T; 5 U; 11 Other;

Query Match 62.1%; Score 18; DB 3; Length 29;

Best Local Similarity .100.0%; Pred.No. 2.1;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUUCUUNNGUAAGCCNANGNG 27

DB 4 GAUUCUUNNGUAAGCCNANGNG 27

RESULT 2

AAA70829
ID AAA70829 standard; RNA; 29 BP.
XX AC
XX AAA70829;
XX 27-APR-2001 (first entry)
XX Molecular interaction site RNA #29.
XX Modulator; identification; molecular interaction; virtual library; ss.
XX Mus sp.
XX WO9558947-A2.
XX 18-NOV-1999.
XX 12-MAY-1999; 99WO-US010361.
XX 12-MAY-1998; 98US-00076404.
XX 12-MAY-1998; 98US-0085092P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX Claim 235; Page 235; 405pp; English.

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating in silico a virtual library of compounds

CC predicted or calculated to interact with the molecular interaction site;
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
 CC with members of the virtual library of compounds to generate a hierarchy
 CC of the compounds ranked in accordance with their respective ability to
 CC form physical interactions with the molecular interaction site. The
 CC method also describes (1) RNA comprising a joined sequence of at least 24
 CC nucleotides but not more than 70 nucleotides and having secondary
 CC structure defined by: (a) 3 nucleotides forming a first side of a first
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
 CC internal loop region; (c) 4 nucleotides forming a first side of a second
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 CC nucleotides forming a second side of the second ds region; (f) 4
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
 CC and isolated RNA fragment comprising the human sequence
 CC UUUACACAUUUCUUAUACGAAAAUUC (II). The methods and products can be
 CC used for identifying agents which modulate the activity of biomolecules,
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds
 XX
 SQ Sequence 29 BP; 8 A; 6 C; 6 G; 0 T; 9 U; 0 Other;

Query Match 62.1%; Score 18; DB 3; Length 29;
 Best Local Similarity 75.0%; Pred. No. 2.1;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GAUUCUUUNNGUAAGCCCNANGNG 27
 |||||
 DB 4 GAUUCUUUNNGUAAGCCCNANGNG 27

RESULT 4
 AAA70828
 ID AAA70828 standard; RNA; 29 BP.
 AC AAA70828;
 XX
 XX 27-APR-2001 (first entry)
 DT Molecular interaction site RNA #28.
 DE Modulator; identification; molecular interaction; virtual library; ss.
 KW Homo sapiens.
 OS WO958947-A2.
 XX
 XX 18-NOV-1999.
 PD 12-MAY-1999; 99WO-US010361.
 XX
 XX 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 XX Hofstadler S, McNeil J;
 PI WPI; 2000-086439/07.
 DR
 XX
 XX Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX
 XX Claim 235; Page 235; 405pp; English.

XX This invention describes a novel method for identifying compounds which
 XX modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds
 CC predicted or calculated to interact with the molecular interaction site;

CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
 CC with members of the virtual library of compounds to generate a hierarchy
 CC of the compounds ranked in accordance with their respective ability to
 CC form physical interactions with the molecular interaction site. The
 CC method also describes (1) RNA comprising a joined sequence of at least 24
 CC nucleotides but not more than 70 nucleotides and having secondary
 CC structure defined by: (a) 3 nucleotides forming a first side of a first
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
 CC internal loop region; (c) 4 nucleotides forming a first side of a second
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 CC nucleotides forming a second side of the second ds region; (f) 4
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
 CC and isolated RNA fragment comprising the human sequence
 CC UUUACACAUUUCUUAUACGAAAAUUC (II). The methods and products can be
 CC used for identifying agents which modulate the activity of biomolecules,
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds
 XX
 SQ Sequence 29 BP; 5 A; 5 C; 7 G; 0 T; 12 U; 0 Other;

Query Match 62.1%; Score 18; DB 3; Length 29;
 Best Local Similarity 75.0%; Pred. No. 2.1;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GAUUCUUUNNGUAAGCCCNANGNG 27
 |||||
 DB 4 GAUUCUUUNNGUAAGCCCNANGNG 27

RESULT 4
 AAA70830
 ID AAA70830 standard; RNA; 29 BP.
 AC AAA70830;
 XX
 XX 27-APR-2001 (first entry)
 DT Molecular interaction site RNA #30.
 DE Modulator; identification; molecular interaction; virtual library; ss.
 KW Rattus sp.
 OS WO958947-A2.
 XX
 XX 18-NOV-1999.
 PD 12-MAY-1999; 99WO-US010361.
 XX
 XX 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 XX Hofstadler S, McNeil J;
 PI WPI; 2000-086439/07.
 DR
 XX
 XX Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX
 XX Claim 235; Page 235; 405pp; English.

XX This invention describes a novel method for identifying compounds which
 XX modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds
 CC predicted or calculated to interact with the molecular interaction site;
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA

nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4 nucleotides forming a second side of the first ds region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified and isolated RNA fragment comprising the human sequence UUUACACAUAUUCAGUUAACAGAAAAC (II). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds

Sequence 42 BP: 12 A: 7 C: 6 G: 0 T: 17 U: 0 Other: xx so

Query Match 62.1%; Score 18; DB 3; Length 42;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 18: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY
4 GAUNCUUNNGUAAGCCCNANGG 27

Dd
7 GAUCUUTUUGUAAGCCCUACGGG 30

RESULT 9	
AAA71124	
ID	AAA71124 standard; DNA; 42 BP.
XX	
XX	AAA71124;
XX	
XX	27-APR-2001 (first entry)
DT	
XX	
XX	Molecular interaction site DNA #130.
DE	
XX	
XX	Modulator; identification; molecular interaction; virtual library; ss.
KW	
XX	
XX	Unidentified.
OS	
XX	
XX	WO9958947-A2.
FN	
XX	
XX	18-NOV-1999.
PD	
XX	
XX	12-MAY-1999; 99WO-US010361.
PF	
XX	
XX	12-MAY-1998; 98US-00076404.
PR	
XX	12-MAY-1998; 98US-0085092P.
XX	
XX	(ISIS-) ISIS PHARM INC.
PA	
XX	
XX	Eker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI	
PI	Hofstadler S, Mcneil J;
XX	
XX	WPI; 2000-086439/07.
DR	

xx Identifying compounds which modulate activity of target biomolecules,
 pt used to provide compounds which can be used as pharmacological,
 pt agricultural and industrial compounds.

Example 7: Fig 125: 405pp; English: PS

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating *in silico* a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary

structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified and isolated RNA fragment comprising the human sequence UUUACAAUACUAGUUUACAGAAAUAUC (II'). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds

Sequence 42 BP: 11 A; 10 C; 7 G; 14 T; 0 U; 0 Other; XX
SQ

Query Match	62.1%	Score 18	DB 3	Length 42
Best Local Similarity	54.2%	Pred. No. 2.2		
Matches 13	Conservative	5	Mismatches 6	Indels 0
	Gaps	0		

QY 4 GAUNCUUNNGUAAGCCCNANGNG 27
||:|::|:|||||:|:|
Dh 7 GATCCTTCTGTAAAGCCCTACGGG 30

RESULT 10	
AAA71132	
ID	AAA71132 standard; RNA; 42 BP.
XX	
AC	AAA71132;
XX	
AC	27-APR-2001 (first entry)
XX	
DE	Molecular interaction site RNA #201.
XX	
DE	Molecular interaction; molecular interaction; virtual library; ss.
XX	
KW	
XX	
OS	Unidentified.
XX	
XX	WO9958947-A2.
XX	
XX	18-NOV-1999.
XX	
XX	12-MAY-1999; 99WO-US010361.
PF	
XX	
PR	12-MAY-1998; 98US-00076404.
PR	12-MAY-1998; 98US-0085092P.
XX	
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
XX	Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI	Hofstadler S, Mcneil J;
PI	
XX	
XX	WPI: 2000-086439/07.
DR	

XX Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.

XX
ps Example 7: Fig 126: 405pp: English.

xx This invention describes a novel method for identifying compounds which
cc modulate the activity of a target biomolecule. The method uses 3-
cc dimensional representations of the biomolecule and a library of compounds
cc and comprises (a) identifying at least one molecular interaction site of
cc the target RNA; (b) generating *in silico* a virtual library of compounds
cc predicted or calculated to interact with the molecular interaction site;
cc and (c) comparing 3-dimensional (3-D) representations of the target RNA
cc with members of the virtual library of compounds to generate a hierarchy
cc of the compounds ranked in accordance with their respective ability to
cc form physical interactions with the molecular interaction site. The
cc method also describes (1) RNA comprising a joined sequence of at least 24
cc nucleotides but not more than 70 nucleotides and having secondary
cc structure defined by: (a) 3 nucleotides forming a first side of a first

CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAGAAUACUAGUUUACAGAAAUUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
xx
SQ Sequence 42 BP; 12 A; 7 C; 6 G; 17 T; 0 U; 0 Other;

Cy	4	GAUNCUUUNNGUAGGCCNANGNG	27
		: : :	
Dd	7	GATTCCTTTTGTGTAAGCCCTACGGG	30
		: : :	

Query Match 62.8%; Score 18; DB 3; Length 43
Best Local Similarity 54.2%; Score No. 2; 2
Matches 13; Conservative 5; Mismatches 6; Indels

RESULT 14	
AAA71119	
ID	AAA71119 standard; DNA; 42 BP.
XX	
XX	
XX	AAA71119;
XX	
XX	
XX	27-APR-2001 (first entry)
XX	
DE	Molecular interaction site DNA #125.
XX	
XX	Modulator; identification; molecular interaction; virtual library; ss
KW	
XX	
XX	Unidentified.
OS	
XX	
XX	WO9958947-A2.
XX	
XX	18-NOV-1999.
XX	
XX	12-MAY-1999; 99WO-US010361.
XX	
XX	12-MAY-1998; 98US-00076404.
PR	
PR	12-MAY-1998; 98US-0085092P.
XX	
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
XX	
PI	Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI	Hoistadler S, Mcneil J;
XX	
XX	
DR	WPI; 2000-086439/07.

Identifying compounds which modulate activity of target biomolecules,
used to provide compounds which can be used as pharmacological,
agricultural and industrial compounds.
Example 7: Fig 125: 405pp: English.

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating in silico a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first internal loop region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second region; (f) 4

CC or industrial compounds
XX Sequence 44 BP; 7 A; 4 C; 5 G; 0 T; 6 U; 22 Other;
SQ Query Match 62.1%; Score 18; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAGCCCNANGNG 27
DB 8 GAUNCUUNNGUAGCCCNANGNG 31
RESULT 23
AAA71125
ID AAA71125 standard; RNA; 44 BP.
XX
AC AAA71125;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #194.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
PN WO9958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
XX WPI; 2000-086439/07.
DR
XX Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
XX Example 7; Fig 126; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; and (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACACAUUAUCUUAUACAAAAC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds

XX
SQ Sequence 44 BP; 7 A; 4 C; 5 G; 0 T; 6 U; 22 Other;
Query Match 62.1%; Score 18; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAGCCCNANGNG 27
DB 8 GAUNCUUNNGUAGCCCNANGNG 31
RESULT 24
AAA71133
ID AAA71133 standard; RNA; 44 BP.
XX
AC AAA71133;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #202.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
PN WO9958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
XX WPI; 2000-086439/07.
DR
XX Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
XX Example 7; Fig 127; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; and (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACACAUUAUCUUAUACAAAAC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds

SQ Sequence 44 BP; 7 A; 4 C; 5 G; 0 T; 6 U; 22 Other;
Query Match 62.1%; Score 18; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUNCUUUNGUAGCCCNANGNG 27
|||||
Db 8 GAUNCUUUNGUAGCCCNANGNG 31
|||||

RESULT 25
AAA70826
ID AAA70826 standard; RNA; 45 BP.
XX
AC AAA70826;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #26.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Rattus sp.
XX
PN WO9558947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Claim 22; Page 232; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; and (g) 3
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACACAUACUAGUACGAAAAC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 45 BP; 14 A; 7 C; 9 G; 0 T; 15 U; 0 Other;

Query Match 62.1%; Score 18; DB 3; Length 45;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GAUNCUUUNGUAGCCCNANGNG 27
|||||
Db 21 GAUUCUUUUUGAAGCCCAAGGG 44
|||||

RESULT 26
AAA70825
ID AAA70825 standard; RNA; 45 BP.
XX
AC AAA70825;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #25.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Mus sp.
XX
PN WO9558947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Claim 22; Page 232; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming an end loop region; (e) 4
CC ds region; (d) 4 or 5 nucleotides forming a second side of the second
CC nucleotides forming a second side of the second ds region; and (g) 3
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACACAUACUAGUACGAAAAC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 45 BP; 14 A; 7 C; 9 G; 0 T; 15 U; 0 Other;

Matches	13;	Conservative	5;	Mismatches	6;	Indels	0;	Gaps	0;
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QY 4 GAUNCUUNGUUAAGCCCNANGNG 27
||: ||:: |:||||| | | |
Db 22 GATTCTTTTGTAAAGCCCCAAGGG 45

RESULT 29
AAA71094
ID AAA71094 standard; DNA; 46 BP.
XX
AC
XX AAA71094;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site DNA #117.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
PN WO958947-A2.
XX
XX 18-NOV-1999.
XX
PP 12-MAY-1999; 99WO-US010361.
XX
XX 12-MAY-1998; 98US-00076404.
PR 12-MAY-1998; 98US-0085092P.
XX
XX (ISIS-) ISIS PHARM INC.
PA
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
XX WPI; 2000-086439/07.
DR

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating in silico a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified and isolated RNA fragment comprising the human sequence UUUACAUAUAUUGUUUACAGAAUAUC (VII). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds

Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 54.2%; Pred. No. 2.2;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0

Qy 4 GAUNCUUUNNGUAAGCCCNANGNG 27
||| : | :: : ||| | | |
Dβ 22 GATTCCTTTTGTAAAGCCCTAGGCG 45

RESULT 30
AAA71085
ID AAA71085 standard; DNA; 46 BP.
XX AC
XX AAA71085;
XX 27-APR-2001 (first entry)
XX DT
XX DE Molecular interaction site DNA #108.
XX DE
XX Modulator; identification; molecular interaction; virtual library; ss.
XX KW
XX Unidentified.
XX OS
XX WO958947-A2.
XX PN
XX 18-NOV-1999.
XX PD
XX PF 12-MAY-1999; 99WO-US010361.
XX PF
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PR
XX PA (ISIS-) ISIS PHARM INC.
XX PA
XX PI Ecker DV, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX PI Hofstadler S, Mcneil J;
XX PI
XX DR
XX DR WPI; 2000-086439/07.
XX PT
XX PT Identifying compounds which modulate activity of target biomolecules.
XX PT used to provide compounds which can be used as pharmacological,
XX PT agricultural and industrial compounds.
XX PS
XX PS Example 7: Fig 121: 405pp; English.

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating *in silico* a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA, with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified and isolated RNA fragment comprising the human sequence UUUACAAUUAUCUGGUUACAGAAAUAUC (II). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds.

Serquence 46 BP: 12 A: 7 C: 9 G: 18 T: 0 U: 0 Other:

```

Query Match          62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 54.2%; Pred. No. 2.2;
Matches 13: Conservative 5; Mismatches 6; Indels 0; Gaps 0;

```

XX
S0
Sequence 46 BP: 12 A: 7 C: 9 G: 18 T: 0 U: 0 Other: 0

Db 22 GAUCCUUCUGUAAAGCCUACGGG 45

RESULT 34
AAA71106
ID AAA71106 standard; RNA; 46 BP.
XX
AC AAA71106;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #182.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
FN WO958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Example 7; Fig 122; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming an end loop region; (e) 4
CC ds region; (d) 4 or 5 nucleotides forming a second side of the second ds
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC nucleotides forming a second side of the first ds region; (e) 4
CC and isolated RNA fragment comprising the human sequence
CC UUUACACAUAAUCUUAAGCCUACGGG (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 46 BP; 14 A; 7 C; 9 G; 0 T; 16 U; 0 Other;

Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GAUCCUUCUGUAAAGCCUACGGG 27
|||:::|:|||||
Db 22 GAUCCUUCUGUAAAGCCUACGGG 45

Db 22 GAUCCUUCUGUAAAGCCUACGGG 45

RESULT 33
AAA71095
ID AAA71095 standard; DNA; 46 BP.
XX
AC AAA71095;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site DNA #118.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
FN WO958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Example 7; Fig 121; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; and (g) 3
CC nucleotides forming a second side of the internal loop region; (2) a purified
CC nucleotides forming a second side of the first ds region; (e) 4
CC and isolated RNA fragment comprising the human sequence
CC UUUACACAUAAUCUUAAGCCUACGGG (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 46 BP; 9 A; 11 C; 9 G; 17 T; 0 U; 0 Other;

Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 54.2%; Pred. No. 2.2;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 GAUCCUUCUGUAAAGCCUACGGG 27
|||:::|:|||||
Db 22 GAUCCUUCUGUAAAGCCUACGGG 45

```
RESULT 35
AAA71107
ID AAA71107 standard; RNA; 46 BP.
XX
XX
AC AAA71107;
XX
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #183.
XX
XX Modulator; identification; molecular interaction; virtual library; ss.
XX
XX Unidentified.
XX
XX WO9958947-A2.
XX
XX 18-NOV-1999.
XX
XX 12-MAY-1999; 99WO-US010361.
XX
XX 12-MAY-1998; 98US-00076404.
XX
XX 12-MAY-1998; 98US-0085092P.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX
XX Hofstadler S, Mcneil J;
XX
XX WPI; 2000-086439/07.
XX
XX Identifying compounds which modulate activity of target biomolecules,
XX
XX used to provide compounds which can be used as pharmacological,
XX
XX agricultural and industrial compounds.
XX
XX Example 7; Fig 122; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
XX
XX modulate the activity of a target biomolecule. The method uses 3-
XX
XX dimensional representations of the biomolecule and a library of compounds
XX
XX and comprises (a) identifying at least one molecular interaction site of
XX
XX the target RNA; (b) generating in silico a virtual library of compounds
XX
XX predicted or calculated to interact with the molecular interaction site;
XX
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX
XX with members of the virtual library of compounds to generate a hierarchy
XX
XX of the compounds ranked in accordance with their respective ability to
XX
XX form physical interactions with the molecular interaction site. The
XX
XX method also describes (1) RNA comprising a joined sequence of at least 24
XX
XX nucleotides but not more than 70 nucleotides and having secondary
XX
XX structure defined by: (a) 3 nucleotides forming a first side of a first
XX
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX
XX internal loop region; (c) 4 nucleotides forming an end loop region; (e) 4
XX
XX ds region; (d) 4 or 5 nucleotides forming a second side of a second
XX
XX ds region; (f) 4 or 5 nucleotides forming a second side of a second
XX
XX ds region; (g) 3 nucleotides forming a second side of the internal loop region; and (g) 3
XX
XX nucleotides forming a second side of the first ds region; (2) a purified
XX
XX nucleotides forming a second side of the first ds region; (2) a purified
XX
XX and isolated RNA fragment comprising the human sequence
XX
XX UUUACACAUAUCUUAUACAGAAAUC (ii). The methods and products can be
XX
XX used for identifying agents which modulate the activity of biomolecules,
XX
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX
XX or industrial compounds
XX
XX
XX Sequence 46 BP; 14 A; 7 C; 9 G; 0 T; 16 U; 0 Other;
XX
SQ
Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUUCUUUNGUAGCCCNANGNG 27
DB 22 GAUUCUUUNGUAGCCCNAGG 45
```

```
RESULT 36
AAA71109
ID AAA71109 standard; RNA; 46 BP.
XX
XX
AC AAA71109;
XX
XX
DT 27-APR-2001 (first entry)
XX
XX Molecular interaction site RNA #185.
XX
XX Modulator; identification; molecular interaction; virtual library; ss.
XX
XX Unidentified.
XX
XX WO9958947-A2.
XX
XX 18-NOV-1999.
XX
XX 12-MAY-1999; 99WO-US010361.
XX
XX 12-MAY-1998; 98US-00076404.
XX
XX 12-MAY-1998; 98US-0085092P.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX
XX Hofstadler S, Mcneil J;
XX
XX WPI; 2000-086439/07.
XX
XX Identifying compounds which modulate activity of target biomolecules,
XX
XX used to provide compounds which can be used as pharmacological,
XX
XX agricultural and industrial compounds.
XX
XX Example 7; Fig 122; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
XX
XX modulate the activity of a target biomolecule. The method uses 3-
XX
XX dimensional representations of the biomolecule and a library of compounds
XX
XX and comprises (a) identifying at least one molecular interaction site of
XX
XX the target RNA; (b) generating in silico a virtual library of compounds
XX
XX predicted or calculated to interact with the molecular interaction site;
XX
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX
XX with members of the virtual library of compounds to generate a hierarchy
XX
XX of the compounds ranked in accordance with their respective ability to
XX
XX form physical interactions with the molecular interaction site. The
XX
XX method also describes (1) RNA comprising a joined sequence of at least 24
XX
XX nucleotides but not more than 70 nucleotides and having secondary
XX
XX structure defined by: (a) 3 nucleotides forming a first side of a first
XX
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX
XX internal loop region; (c) 4 nucleotides forming an end loop region; (e) 4
XX
XX ds region; (d) 4 or 5 nucleotides forming a second side of a second
XX
XX ds region; (f) 4 or 5 nucleotides forming a second side of a second
XX
XX ds region; (g) 3 nucleotides forming a second side of the internal loop region; and (g) 3
XX
XX nucleotides forming a second side of the first ds region; (2) a purified
XX
XX nucleotides forming a second side of the first ds region; (2) a purified
XX
XX and isolated RNA fragment comprising the human sequence
XX
XX UUUACACAUAUCUUAUACAGAAAUC (ii). The methods and products can be
XX
XX used for identifying agents which modulate the activity of biomolecules,
XX
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX
XX or industrial compounds
XX
XX
XX Sequence 46 BP; 9 A; 11 C; 9 G; 0 T; 17 U; 0 Other;
XX
SQ
Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUUCUUUNGUAGCCCNANGNG 27
DB 22 GAUUCUUUNGUAGCCCNAGG 45
```

RESULT 37


```
XX AAA71096;
AC 27-APR-2001 (first entry)
XX Molecular interaction site DNA #119.
DE Modulator; identification; molecular interaction; virtual library; ss.
XX Unidentified.
XX WO9958947-A2.
XX 18-NOV-1999.
XX 12-MAY-1999; 99WO-US010361.
XX 12-MAY-1998; 98US-00076404.
XX 12-MAY-1998; 98US-0085092P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX Example 7; Fig 121; 405pp; English.
XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds
XX predicted or calculated to interact with the molecular interaction site;
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX with members of the virtual library of compounds to generate a hierarchy
XX of the compounds ranked in accordance with their respective ability to
XX form physical interactions with the molecular interaction site. The
XX method also describes (1) RNA comprising a joined sequence of at least 24
XX nucleotides but not more than 70 nucleotides and having secondary
XX structure defined by: (a) 3 nucleotides forming a first side of a first
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX internal loop region; (c) 4 nucleotides forming a first side of a second
XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX nucleotides forming a second side of the second ds region; and (f) 3
XX nucleotides forming a second side of the internal loop region; and (g) 3
XX nucleotides forming a second side of the first ds region; (2) a purified
XX and isolated RNA fragment comprising the human sequence
XX UUUACACAAUACUAGUUACAGAAAAC (II). The methods and products can be
XX used for identifying agents which modulate the activity of biomolecules,
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX or industrial compounds
XX
SQ Sequence 46 BP; 11 A; 7 C; 9 G; 19 T; 0 U; 0 Other;
Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 54.2%; Pred. No. 2.2;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAGCCCNANGNG 27
DB 22 GATTCCTTTTGTAGCCCTAGGGG 45
RESULT 40
AAA71099
ID AAA71099 standard; DNA; 46 BP.
XX
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AC AAA71099;
XX 27-APR-2001 (first entry)
XX Molecular interaction site DNA #122.
XX Modulator; identification; molecular interaction; virtual library; ss.
XX Unidentified.
XX WO9958947-A2.
XX 18-NOV-1999.
XX 12-MAY-1999; 99WO-US010361.
XX 12-MAY-1998; 98US-00076404.
XX 12-MAY-1998; 98US-0085092P.
XX (ISIS-) ISIS PHARM INC.
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Query Match 62.1%; Score 18; DB 3; Length 46;
Best Local Similarity 54.2%; Pred. No. 2.2;
Matches 13; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAGCCCNANGNG 27
DB 22 GATTCCTTTTGTAGCCCTAGGGG 45
Search completed: April 18, 2004, 08:03:33
Job time : 217.667 secs
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